

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

(A) NAME : I.N.S.E.R.M
(B) STREET : 101, rue de Tolbiac
(C) CITY : PARIS CEDEX 13
(E) COUNTRY : FRANCE
(F) POSTAL CODE (ZIP) : 75654

(A) NAME : Max-Planck-Gesellschaft zur Förderung
des Wissenschaften e. V., Berlin
(B) STREET : Hofgartenstrasse 2
(C) CITY : München
(E) COUNTRY: Germany
(F) POSTAL CODE (ZIP) : 80539

(A) NAME : SMITHKLINE BEECHAM
(B) STREET: New Horizons Court
(C) CITY : Brentford
(D) COUNTY: Middlesex
(E) COUNTRY : Great-Britain
(F) POSTAL CODE (ZIP) : TW 89 EP

(ii) TITLE OF THE INVENTION: DNA, specific proteins and peptides of the Neisseria meningitidis species bacteria, methods for obtaining them and their biological application.

(iii) NUMBER OF SEQUENCES: 99

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (OEB)

(2) INFORMATION FOR SEQ ID NO: 1:

09928457-081401

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) TYPE DE MOLECULE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GATCCGCTGC CGGCAGACGA ATATCAAGAC ATCTTCGATT TTATGAAACA GTATGACTTG	60
TCTTACCCGT ATGAATATCT GCAGGATTGG ATAGATTACT ATACGTTCAA AACCGATAAG	120
CTGGTATTTG GTAACGCGAA GCGAGAGTGA GCCGTAAAC TCTGAGCTCC TGTTTTATAG	180
ATTACAACCT TAGGCCGTCT TAAAGCTGAA AGATTTTCGA AAGCTATAAA TTGAAGCCCT	240
TCCACAGTAC ATAGATC	257

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) TYPE DE MOLECULE: DNA (genomic)

(vi) ORIGIN:

09923457.081401

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GATCATGTTT AAATAGATAG GCATGGGAAG CTGCAGCTCT AACGTCCATG AAAATATGTT	60
GCATAGCTGC AAGCGGAACG CCTTTTCTTT CATCTACATA ATCTATAGAG TCAAGGCAAC	120
CGCTATTGAA ATTAGCAGTA TTGCCTATGA TTACATTAGT AATATGCTCA TACCATTTTT	180
GGGTGGTCAT CATATTGTGC CCCATTGTTA TCTCCTTATA TTGGTTTTAG AAGGAACTTT	240
GACAGGAAGA ATAACGGCCT TACCTGTTTG ACGATC	276

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 428 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GATCTGGTGG TGTTCACACA GGTAGGCGCA TACTTGTTTCG GGAAGTGGTT TGCGGCGGAT	60
AAGGGTGTCTG ATGTGCTGAA TCAGCTGCGA ATCGAGCTTA TAGGGTTGTC GCTTACGCTG	120
TTTGATAGTC CGGCTTTGCC GCTGGGCTTT TTCGGCGCTG TATTGCTGCC CTTGGGTGCG	180

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GTGCCGTCTG ATTCGCGGC TGATGGTGCT TTTGTGGCGG TTAAGCTGTT TGGCGATTTC 240
 GGTGACGGTG CAGTGGCGGG ACAGGTATTG GATGTGGTAT CGTTCGCCTT GGGTCAGTTG 300
 CGTGTAGCTC ATGGCAATCT TTCTTGCAGG AAAGGCCGTA TGCTACCGCA TACTGGCCTT 360
 TTTCTGTTAG GGAAAGTTGC ACTTCAAATG CGAATCCGCC GACCTCTTTC AGTTACAGCA 420
 GCTTGATC 428

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : *Neisseria meningitidis*
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GATCCTGCAT TGACATCGGC CTTGGCTGTC AGGGTATTGT GACCGGTAAA GTCGGCATT A 60
 CCGTTGGCCA ATAAGGATAC ATGACCGTCT GCAGAAACAG CATGAAGGCC GTCTGAAACG 120
 ATATTGCCCT GCAATGCGGT GGTTTCGAGA GCCTTGGCTG CGTTCAGCTT GGTATTGCGA 180
 AGCTGAATAT TGCCTTTGGC TGCCTGAATG TGCAGATTAC CCGAGTTGGT ACGCAGATTG 240
 GTATTGGTAA CATTGAGCAA GCCTGCCTCC ACACCCATGT CTTTGTAGGC AGTGAGGGTT 300
 TTA CTGGTGC CGGTAATATG GGCAGCGTTA TCCGATTTC AATGGATGCT GGCCGGCAGA 360

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CAAATCTTTA TCAACATTCA AATTCAGATC

390

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GATCAGATTG GTGAAGACGG TATTACCGTC AATGTTGCAG GCCGTTCTGGG ATATACGGCG	60
AAAATCGACG TGTCTCCGAG TACCGATTTC GCGGTTTATG GCCATATTGA AGTTGTACGG	120
GGTGCAACGG GGTGACCCA ATCCAATTCA GAGCCGGGTG GAACCGTCAA TTTGATC	177

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGIN:

- (A) ORGANISM : *Neisseria meningitidis*
 (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GATCAATGAT GCTACTATTC AAGCGGGCAG TTCCGTGTAC AGCTCCACCA AAGGCGATAC 60
 TGAATTGGGT GAAAATACCC GTATTATTGC TGAAAACGTA ACCGTATTAT CTAACGGTAG 120
 TATTGGCAGT GCTGCTGTAA TTGAGGCTAA AGACACTGCA CACATTGAAT CGGGCAAACC 180
 GCTTTCCTTA GAAACCTCGA CCGTTGCCTC CAACATCCGT TTGAACAACG GTAACATTAA 240
 AGGCGGAAAG CAGCTTGCTT TACTGGCAGA CGATAACATT ACTGCCAAAA CTACCAATCT 300
 GAATACTCCC GGCAATCTGT ATGTTCATAC AGGTAAAGAT C 341

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
 (B) TYPE : nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : *Neisseria meningitidis*
 (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GATCCAAC TG TTTGATTTTA CTGGCTGCTT CTCCATGCGC GGTATTGACC AAAGCCGCAA 60
 GGATATTGCG TTCCAGATTG TCTTTCAGGC TGCCGCCGTT GACAGCGGTA TTAATCAGTG 20

09923457.081404
 104180.75432650

CGGCACTGCC CGCATTTGGCT AGGTTGACGG TCAGGTTGTT GATC

164

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GATCAATCAC ACATCTTGTC ATTTTTTCGA TTCCTTCATT TCGGTTTCTA ATGTTTCAAT	60
TCTTGCGGCC ATTTCTTGAA TGGCTTTAGT CAAAACGGGG ATGAACGCTT CGTATTCGAC	120
GGTGTAGGTA TCGTTTGTTT TATTTACCAT CGGCAATCGA CCATATTCAT CTTCCAGCGC	180
AGCAATGTCC TGGGCAATAA ACCAATGCCG CAACCGATC	219

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

09928457.081401

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GATCTTGGGT AAGCCCCCAA CCTGCATAGA AAGGCAGGCC GTAGCAGCTG ACTTTTTTGC	60
CGCGCAACAA GGCTTCAAAA CCGGTCAGCG AAGTCATGGT ATGTATTTTCG TCTGCGTATT	120
GGAGACAGGT CAGGATGTCG GCTTGTTTCGG CGGTTTGGTC GGCATATCGT GCAGCATCAT	180
CAGGGGAAAT ATGGCCGATG CGGTTACCGC TGA CTACATC GGGATGCGGT TTGTAGATGA	240
TATAGGCATT GGGGTTTCGT TCGCGTACGG TACGGAGCAA ATCCAGATTG CGGTAGATTT	300
GGGGCGAACC GTAGCGGATA GACGCATCAT CTTCAACCTG GCCGGGAACG AGGATC	356

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GATCCGCTTT CAGTTTCCGT ACCGGTGGCA TCACTCAAGT CCGTTTTGTG CACCAAACCG	60
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CGTCCATATG AAACATAAAA CAAATCGCTT AAGCCCAAAG GGTATATCGAA CGATAAAGCG 120

ACATTTCCCTT GATATTTGCC GGTCTGTTTG CCGCCCGCAT CATCTATACC GATACTGAAC 180

CGTATGGGTT TATTCTGCTG CCATTTGATC 210

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GATCCCGAAA CGCAATTGGT CGAAAGCTAT ATGCTGAACG ATGTGTTGCG GTTTTGGGAC 60

AGCGCAGGTT TGGGCGATGG GAAAGAAGCC GACCGCGCCC ATCGGCAAAA ACTGATTGAT 120

GTCCTGTCTA AAACCTATAC TCATTCCGAT GGGCAGTGGG GCTGGATAGA TTTGGTGTTT 180

GTATATCCTTG ACGGCAGCTC CCGCGATTTG GGTACGGCCT ATGATTTGTT GAGGGATGTT 240

ATCCTTAAAA TGATTGATC 259

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single

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(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GATCAAATGG ATGATTTATA TAGAATTTTC TTTTACGACT GCGTGCCGTT TGAAAAGAAA	60
ATGCACAATC CCGTATCTCA TCGTGCCATA GATTTTTTCAA AGACTCCGGA AGCCATATTT	120
CGTTGCAATC TGCATACCGA ATTGAAGAAG AAGCGTAAAT TAGCGTTACG TTTAGGCAAG	180
CTGTCGGACA ATACAGCATG GATATTAAAA CCCCAAGTCA TGAAAAATCT TCTGAAAAAC	240
CCGTCAACTC AAATTACGGA AAACGATGTC GTGCTCGATG TTAAACAAAA AGGTGTAGAT	300
ATGCGTATAG GCTTGGATAT TTCATCTATT ACCTTAAAAA AACAAGCCGA TAAAATCATC	360
TTGTTTTCTG GTGATTCCGA TTTTGTCCCA GCAGCCAAAT TAGCCAGACG GGAAGGTATC	420
GATTTTATTC TTGATC	436

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

09923457.081401

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GATCGTTTTA CGTCGCAATC GAGCTTTGTG GTGCGCTCGC CTAAAAGCCA ATCTTCTCTC 60
 AATGGCCTGG GTGCCATTTT GCAGGGCACA GGTTTTGCCC GTGCGCAAGA CGATATTTAT 120
 ACCGTGCAGG AATATATGCA GTCGCGTTCG GCTTTGGATG CGTTGCGTAA GAAAATGCCC 180
 ATTCGCGATT TTTATGAAAA AGAAGGCGAT ATTTTCAGCC GTTTTAATGG TTTTGGCCTG 240
 CGTGGCGAGG ATGAGGCGTT TTATCAATAC TACCGTGATA AGGTATCCAT CCATTTTGAC 300
 TCTGTCTCAG GCATTTCCAA TTTGAGCGTT ACATCGTTTA ATGCCGGTGA ATCTCAAAAG 360
 ATC 363

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : *Neisseria meningitidis*
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GATCTTGCCT CATTTATATC TTCACCGATA TTGCAATTAC CGCCGTTCCA GTTGAAATAA 60

09923457.081401

CAACGACTAA AATTGTAGTT CCTAAAAGAA TCATTCCTAT TCTTGCGTAC CATTTCCCAA 120
 TAATTGCGCC CGACAATTTT CATTTAATGC TCCATCAGTT CTTTACTTC CGGAAATCTG 180
 CTGTAATCTG ACATAAGACG CATAATTGAA CTATCAACGC CGTAACAGCC ATAGGTTTTA 240
 ATACCGTTTT CGGCGTGTTT CCAAATGCAA TTACTGTATT CGTAGCCTTT TACAAATTTA 300
 TCGGTTTCGG GATC 314

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GATCATACGA ATCTACCCTA AAATACCCCG TCGCCGATTT AGGATTGGCT ACATAAAGCT 60
 CATTATAAGG GTATTTTGAT GACATGATAC GGTAAATTC ATTGCCGTTG TTTATCCTGA 120
 TTCTATAAAT TGGTTCAACA GCAAAGCCTC TGGATTCCCT TAATTGATTA TAATATTGCC 180
 TGTATGTTTG TACATCATGT CTTGTCCACG GCTCTCCAGG AGTCCTCAGA ATAGCAATCC 240
 CGTTAAATTT CGGATC 256

09923457.081404

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GATCCACGCC TGTGCCTACC TTGGCTTTTT GTTCGCCAAA CAAGGCATTT AAGGTTGAGG 60

ACTTGCCGAC ACCTGTCGCA CCGACAAGCA AGACATCCAA ATGACGGAAA CCGGCTGCTG 120

TGACTTTTTG CCCGATTTC AAAATACGGT AACGATGCAT ATGCGCTCCT ACCAGCCAAA 180

AAAAGAAGCA ACCGTGCTAA TCGCCCCTCC AATCGCTTTT GCAGCACCGC CGATC 235

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

09928457.081404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GATCCAACGG GCATCGCTGT CCTTACTCGG TGTGGTTTGA CCGCTGATTT GTCCTTCTTC 60
 GTCAACTTCT ATGGCCTGAC GCTGTTTGCT GCCGGCGGTC TGGATAATGG TGGCATCAAC 120
 GACGGCGGCG GATGCTTTCT CTATTTTATAG GCCTTTTTCG GTCAGTTGGC AGTTAATCAG 180
 TTTGAGTAAT TCGGACAGGG TGTCGTCTTG CGCCAGCCAG TTGCGGTAGC GGCATAAGGT 240
 ACTGTAATCG GGGATGATC 259

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GATCTGTGCC GTTGATTTTA TCTTTCAGAT GCAGCATCGA ATATCGGAAA GCCAAATCAG 60
 CAATTCTTTT TGCATCGTGT GGATTTTGAG ACGGGCCTAA TGACCGTACC CGCTTAATAA 120
 AAAATGCACC GTCAATCAAA ATGGCGGTTT TCATATTGCT TCCCCTATAT TTGTCAAAGA 180
 TATAAAAAAG CCCTTGGGAT C 201

09928457-081401
 104180-25482660

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

AATTCAAAGG AGGCATTTGT TGCAAGAAAA GTACAAAGTG ATTTGCAAAA AGCATTGAAT 60
 GCTAGCAACT ATAACAAGCA GCAATATGCA AGACGTGCGG CAACAGCGTT AGAGAATGCT 120
 TCAAAATCAA AAGTTATGGC AGCGAATTCT TTTTGATCTA TCTTGTGCGA ACGGGTCAAA 180
 TATTCTTCGT ACATTGAGTT AATCGTACCA ATCGCCCTAA CCACATTTTC ATCAGAAAAT 240
 ATGGAAATAA TAGCATCCCT ATACGCACCT AGTGTAATAT TGTTTCTATT ATTAGTTATA 300
 GCATTATTCG AATACATAAT AGCACCTCCA AATT 334

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

09928457-081401

(vi) ORIGIN:

- (A) ORGANISM : *Neisseria meningitidis*
 (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AATTCCTGCG CACCTTTGCC GATGGGGAGA TAATCGCCTT TTTGCAGCAT TCTGCCCTGA 60
 TGGCCGCCGA AACCGGCTTT CAGGTCGGTA CTTCTCGAAC CCATCACTTC CGGCACATCA 120
 AATCCGCCCCG CCACGCACAC ATAGCCGTAC ATGCCCTGCA CGGCACGCAC CAGTTTCAAG 180
 GTCTGCCCTT TGCGGGCGGT ATAACGCCAA TACGAATAGA CCGGTTCGCC GTCCAATT 238

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
 (B) TYPE : nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : *Neisseria meningitidis*
 (B) STRAIN : Z2491

(xi) DESCRIPTION DE LA 4SEQUENCE: SEQ ID NO: 21:

AATTGGGCGA GATGCTGCCG GAAACGGATT TAAACAGAT TGCGGCGGCA GTGTTGAAGA 60
 CGAACGATGA GCGGCATTG CAGAAGGTGG TGAAAACGGC CAAAGGCAAT GCGCGGAAAC 120
 TGTCGAAGCT GCTGCTGATT GTGGACTATT TGTTGCAGGT TAACCCTGAT GTTGATTGG 180

09928457.081401
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ATGATGATGT AATCGAACAC GCGGAAACCT ATTTAATCCA CTAAACCTTT GACAGATAAG 240

GCAATAATT 249

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

AATTTATGTA CGGTTTTGCC GTTTCAGTC AGCCAGTCGG CAAGGCGCAG AAAAAAATCG 60

CCGACAGGGC CTTGAAGCAG CAGGATATTT TCTGCGCTTT CAAGCAGGTT TTGCAGGTTA 120

TTTTTGAGGA CGGTCTGTTT CATGTTGCAA TGTGGTTTTG TTTTTTATGT AATAGTTTAA 180

GGTTGAACTT TCAAGCATAC GCCAAGAGAA TT 212

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single

09928457.081401

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

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AATTCAGTGC CTGCGTCATA TCACGGCTAC CTTGTGGTTC AGGGTTACTG TATCGCCCGC      60
GGCATCGACG GCTTCAATAT GCAGCTTCAG CCAGCCGTGC TCGGGGGCGG ATGCGGTTAC      120
TTGGATGGAT TGGGCGCGTT TGGACTGAAT CACGGGCTGC AAGGCTTGCT CGGCGTACTG      180
TTTGGCCAGT ACTTCGATGC GCTTTAAATG CTTTGGCGG CGCAATT                      227

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(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

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GATCCAGGAC TCAAAAACCG ATTTCTAAT AGAGTGTCTA ATATCCCAAT CTTTTTACC      60

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09923457.081401

CCCTCTGCTG TAGAATTGAT AGAGAAAGTT TGTCTATCTT TTTCATATAC CCATGCCTTC 120

TTTTTATCAT TGTAGCTAAC ATAACCGCCA AACAAATGCTT CTAGATC 167

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AATTCTTGCG GCCATTTCTT GAATGGCTTT AGTCAAAACG GGGATGAACG TTTCGTATTTC 60

GACGGTGTAG GTATCGTTTG TTTTATTTAC CATCGGCAAT CGACCATATT CATCTTCCAG 120

CGCAGCAATG TCCTGGGCAA TAAACCAATG CCGCAACCGA TCTTCTTTAT GACTGCCGTC 180

CTTGATTGGA TTCGCCCACC ATTCGCGGAC TTTGTCCGCT CGTTCATCTG CCGGCAAGTC 240

TTTGAATAAT T 251

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs

09928457.081401

- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

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AATCCCGAC TATCGCGGAT GCGTAGTTTT TGCCGGTGGG CAAGAGCAGG TGTGGGATAA      60
GTTAGGTGAT TTGCCCAGATG GCGTCAGCCT GACCCCGCCT GAATCGGTAA ATATTGACGG      120
CTTAAAATCC GTAAACTCG TCGCATTAAA TGCTGCCGCT CAGGCTTTTA TTAACAAGCA      180
CGCCGGTATC GACAGCGTAC CTGAATT                                           207

```

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

09928457.081401

AATTGTTTGG GAATAATCCA AACAAACAGC ATCAGGATAG CGGCGGCGGT CAGGCTGCCT 60
 GAAAGGATTT TGCCGGGGTT TTTTGTAGGC AAAGCGGACG AGAAACCAA GCAACAGCAG 120
 CATGGTGTCC CAATAGCCGA TTGAGAATAG GATGGCCAAA CCTTCTAGGA AATGGCGTAA 180
 ATCGTTTGTG GTAACCATGG GTAGTTCCTG TGGTTAAATG TGCAGGCTGC TTTTGGCCGA 240
 ACCTTGCCGC ATCTCAAAAAG CAGCCTGCGC TTCAGCGTTG CGTTACGCAG TAAAATAATG 300
 AATATTTGTA ACGGCTTGGG TATTTTTTGT CAATATTCCC GCCCTTCCCT TAACAGCTGC 360
 CGCGCTTTCC GTTAAAAATT 379

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

AATTCGCCGA AATCAGGCTG CTGCTCGATA ATCGGCGCGG CCGATTGGCG TTGTGCCTCG 60
 ATTAAATCCA TCTTGTCTTG CAGACGTTTG GCCTGGCCTT TCGGGCGGCG TTCGGCCAGT 120
 TGTTCATCC GCGTTCCGC AAATGCCGCC CGTTTGTTCG CGTTGAATAC CGCTTTGCAA 180
 ATCACCTTGC CCTGCATATC CTTACAATC ACATGGTCGG CATCGTGGAT GTCGTAAGCC 240

09928457.081401

ACCCGTACCT TCTGACCGCT GTAATCCAGC AATT

274

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

AATTCGGTTC TTATTGGGCT TTTTCCATCC ATCGGGTATG CCTGAAGGGA ACGCAAACCC	60
TGCCACTTGC CCATCGCTCC ATTCCCGCAT TAGCGCGTCT GACGGCAAGT GTTCTCGCGC	120
CCAATCAAGC CACGCCTGCC GCATTGCGGC CTTGTCTGTC TGAAAACTTC GCAGTGCTTT	180
TGCAACCGGC CCATCAATTAA CTTCAATCAA ATAAATCATT ATATTGCGT TCATTTTTCC	240
TACACCTTCG CCACATCCAA ATT	263

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

09923457.081401

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

AATTGTTCAA GAAAAAGTC GGCACGGCGC GGCAACGGGG AAAATGCGTT GACGCCGTCT	60
TTTTCTAAGG TGATGTAGTA GGGGCGGAAA TAGCCTTCTT CAAACGCCCA GAAACTGGCT	120
TGGTTTTTCGT TTGCAATGCG TTTTGCAATG ACGTGATAAG GCGTGTGTC GCCAAAGCAG	180
ACAACGGCCT GGATGTGATG TTGAGTGATG TATTCTTGCA AAAACTCAGG AAAGGCGTCG	240
TAGTTGTCGT TAAAAACAAC GGTATGCGCT TGAGTGGGCG GATAAAAATA GTCGTCGCCT	300
GCATTAAAGT TGAATT	316

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

09928457.081401

AATTCAATCA ACGGAAAACA CATCAGCATC AAAAACAACG GTGGTAATGC CGACTTAAAA 60
 AACCTTAACG TCCATGCCAA AAGCGGGGCA TTGAACATTC ATTCCGACCG GGCATTGAGC 120
 ATAGAAAATA CCAAGCTGGA GTCTACCCAT AATACGCATC TTAATGCACA ACACGAGCGG 180
 GTAACGCTCA ACCAAGTAGA TGCCTACGCA CACCGTCATC TAAGCATTAC CGGCAGCCAG 240
 ATTTGGCAAA ACGACAAACT GCCTTCTGCC AACAAGCTGG TGGCTAACGG TGTATTGGCA 300
 CTCAATGCGC GCTATTCCCA AATT 324

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : *Neisseria meningitidis*
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

AATTATGCAA AAAAACGCAA CGCCGAAAAA CTGGCACCGC GCGGATATTG TTGCTGCTTT 60
 GAAAAAGAAA GGCTGGTCAC TTCGAGCACT TTCAATAGAA GCGGGGTGTG CGCCGAATAC 120
 GCTTAGAAGC GCACTGGCCG CCCCTTATCT TAAGGGAGAA AGGATTATTG CCGCTGCAAT 180
 CGGAGTGGAA CCGGAAGAGA TTTGGTCCGA ACGGTATGCA GATCGGAATT 230

09020457.001401

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

AATTTAATCG GTGGAATGCC TGTTCAACCG CACCAATCCC GCTGAATACG GTTGCTAATC	60
TAATATGTGA ATCAGGTTTA AGAAAAGTTT TAGATTTCCA ACCTTGTTGA CTGGGAAAGA	120
GCAAAGTTTT TTGTAATCGA GTATCGTGTG TCTGTGCCAT TGTCGAAATA GTCATACTTA	180
TATCGTTCTG TTTATCTTAT CAATATGAAA ACTACATCGT TGATTGCCCT GACAATGCCT	240
TGGTCAATT	249

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

09922457.081401

(vi) ORIGIN:

- (A) ORGANISM : *Neisseria meningitidis*
 (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

AATTCTTGTC CCGGAGTCCA ACGTATATTT ACCCTCCTGC GAGCTAAAAG ACTATTATTC 60
 TCCACTGCCA CAGTAGCCGC ATTCACCGCC GTATTCACAT CCCCTTTAAC CAATGCCACT 120
 GCGCTGCCTG CGATAATCTG CGAGTAGGCT ATGACTTTTTT GCGTTCTTG GGGTGACAGT 180
 TTGCCTACAT CGCGTCCGTC CAACAGGGTT TCTCCACCA TCTCGCCGAC TGCCGCGCCG 240
 ATTGCGCCGT CCCGACATTT GCCTTTATTT GCTACCGCCG ATGCACAGCC TGCTACGGCA 300
 TGGGCTATCT TGTGGGCAAT GTAGTCTTCG CTGAGATTAA ATT 343

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
 (B) TYPE : nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : *Neisseria meningitidis*
 (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

AATTCTTCAA ACATCGTTTC GATAATCGGG TCGGTGTACA CACTGATGCG GTCGCCCCGCA 60

09026457-081401
 104180-25482660

CGGCTTTGAC CGGCTCGGAA AATATAGGCG GTGGCTTTGC CGTCGGCGAT GTCGACGCAC 120
 CAACGCCAGA TGGCGTCTTC GGTATTCAAA CAATCACCCG CACAGCTTTC ACCTGCGCGG 180
 AATT 184

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15620 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TATGCTCAAT CTCATTTTCA AAATGCAAAA CTTTCTGAT TTTTCTACT TTTTGCTCAA 60
 TATTAGGAAG GTTTTAGGCA ATTGAAAATT TTTTGGCGCA TTTTATGCG TCAAATTTTCG 120
 TTAACAGACT ATTTTGTCAA AGGTCTCCGT CTGTAAAAGC AAGGATAGGG CATCTGCCCT 180
 TTTGATTGTT TGATTACGA TACAAGGAGT TTCAAAATGA GAGTTTTATA GTGGATTAAAC 240
 AAAAACCAGT ACAGCGTTGC CTCGCCTTGC CGTACTATTT GTACTGTCTG CGGCTTCGTC 300
 GCCTTGTCTT GATTTAAATT TAATCCACTA TATGTGTTCA TGAAATGACT TGGGTCGGAG 360
 GCTCAGGTAA TGCACAACAA AGTTCATATT ATTGCGAAAT TTGCGAATCT GCAGGGCTTA 420
 ACGATACGGG AAATCCTGAT AAATCTTTAG GATTGCCAAA CAATACGTTC AGTAATCCGC 480

09923457.081401

CTGGTTGGGG AGCTACAATC GGAGCTTTAG CAGGTAGCCG CATAGGTATG CCTGAATTTG	540
GTACGTTTGC GAGCCATGCC ATTGAAAATT TCGACTGGTC ATGGTATCGA CGTTATAGGG	600
AAATTGCCGA AACGATTGAA CGAGAATATT CAGGCGGTTT GCCTTAATAG TTGAGGAGGT	660
CATGATGTTT GCCAAACATT ATCAATTCAT CGCACTCGGC ATCATGCTGC TTCTTTATAT	720
GTTGATTCTC TATACGACCG ATTTTTCCAA TCTGACGTAT TGGATGCTGT TTTTATCTG	780
TTTTATTACA GGAAAAATAT TAGCTCGTTT GTTAGAGAAA AGCTTTAAAT AAAATAGCAG	840
CTAGTCGCAA AAGGTCGTCT GAAACCTTTT CAGGCGGCCT TTCTAAAATA CATCCAACCT	900
CCTAATCCCT ATTTTTCAAA AAGGAAATCT ATGCCCCATC TGCAAAACCT GTCTTTGGGC	960
TTAAAGAAAA AGCTGCCTGT TATCCTGCAA ACAGAAATAT CAGAATGCGG CTTGGCATGT	1020
CTGGCGGCTG TGGCGGGATT TCATGGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA	1080
TACTGTCCGA GACCTTTGCA AAATTCCCCA AAATCCCCTA AATGTCTTGG TGGGAATTTT	1140
GGGGAATTTT GCAAAGGTCT CATTCCTATA CTGTAAATAC TTTTAAATTT ATGACAAAAT	1200
AGTAAATATT GCTAAAATAA TATTGATGTC ATGAAATTTT TTCCTGCTCC ATGTCTGTTG	1260
GTTATCCTGG CTGTCATACC CCTTAAAACC TTAGCTGCCG ATGAAAACGA TGCAGAACTT	1320
ATCCGTTCCA TGCAGCGTCA GCAGCACATA GATGCTGAAT TGTTAACTGA TGCAAATGTC	1380
CGTTTCGAGC AACCATTGGA GAAGAACAAT TATGTCCTGA GTGAAGATGA AACACCGTGT	1440
ACTCGGGTAA ATTACATTAG TTTAGATGAT AAGACGGCGC GCAAATTTTC TTTTCTTCCT	1500
TCTGTGCTCA TGAAAGAAAC AGCTTTTAAA ACTGGGATGT GTTTAGGTTT CAATAATTTG	1560

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AGCAGGCTAC AAAAAGCCGC GCAACAGATA CTGATTGTGC GTGGCTACCT CACTTCCCAA	1620
GCTATTATCC AACCACAGAA TATGGATTCTG GGAATTCTGA AATTACGGGT ATCAGCAGGC	1680
GAAATAGGGG ATATCCGCTA TGAAGAAAAA CGGGATGGGA AGTCTGCCGA GGGCAGTATT	1740
AGTGCATTCA ATAACAAATT TCCCTTATAT AGGAACAAAA TTCTCAATCT TCGCGATGTA	1800
GAGCAGGGCT TGGAAAACCT GCGTCGTTTG CCGAGTGTTA AAACAGATAT TCAGATTATA	1860
CCGTCCGAAG AAGAAGGCAA AAGCGATTTA CAGATCAAAT GGCAGCAGAA TAAACCCATA	1920
CGGTTTCAGTA TCGGTATAGA TGATGCGGGC GGCAAAACGA CCGGCAAATA TCAAGGAAAT	1980
GTCGCTTTAT CGTTCGATAA CCCTTTGGGC TTAAGCGATT TGTTTTATGT TTCATATGGA	2040
CGCGGTTTGG TGCACAAAC GGACTTGACT GATGCCACCG GTACGGAAAC TGAAAGCGGA	2100
TCCAGAAGTT ACAGCGTGCA TTATTCGGTG CCCGTAAAAA AATGGCTGTT TTCTTTTAAT	2160
CACAATGGAC ATCGTTACCA CGAAGCAACC GAAGGCTATT CCGTCAATTA CGATTACAAC	2220
GGCAAACAAT ATCAGAGCAG CCTGGCCGCC GAGCGCATGC TTTGGCGTAA CAGGTTTCAT	2280
AAAAC TTCAG TCGGAATGAA ATTATGGACA CGCCAAACCT ATAAATACAT CGACGATGCC	2340
GAAATCGAAG TGCAACGCCG CCGCTCTGCA GGCTGGGAAG CCGAATTGCG CCACCGTGCT	2400
TACCTCAACC GTTGGCAGCT TGACGGCAAG TTGTCTTACA AACGCGGGAC CGGCATGCGC	2460
CAAAGTATGC CCGCACCTGA AGAAAACGGC GGCGGTACTA TTCCAGGCAC ATCCCGTATG	2520
AAAATCATAA CCGCCGATT GGATGCAGCG GCCCCGTTTA TGTGGGCAA ACAGCAGTTT	2580
TTCTACGCAA CCGCCATTCA AGCTCAATGG AACAAAACGC CTTTGGTTGC CCAAGACAAG	2640
TTGTCTATCG GCAGCCGCTA CACCGTTCGC GGATTGATG GGGAGCAGAG TCTTTTCGGA	2700

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GAGCGAGGTT TCTACTGGCA GAATACTTTA ACTTGGTATT TTCATCCGAA CCATCAGTTC	2760
TATCTCGGTG CGGACTATGG CCGCGTATCT GGCGAAAGTG CACAATATGT ATCGGGCAAG	2820
CAGCTGATGG GTGCAGTGGT CGGCTTCAGA GGAGGGCATA AAGTAGGCGG TATGTTTGCT	2880
TATGATCTGT TTGCCGGCAA GCCGCTTCAT AAACCCAAAG GCTTTCAGAC GACCAACACC	2940
GTTTACGGCT TCAACTTGAA TTACAGTTTC TAACCTCTGA ATTTTTTTAC TGATATTTAG	3000
ACGGTCTTTC CTTATCCTCA GACTGTCAAA CTTTACCTAC GTACTTGGCG CGCAGTACGT	3060
TCATCTTCAA AATGGAATAG ACATGAATAA AGGTTTACAT CGCATTATCT TTAGTAAAAA	3120
GCACAGCACC ATGGTTGCAG TAGCCGAAAC TGCCAACAGC CAGGGCAAAG GTAAACAGGC	3180
AGGCAGTTCG GTTTCTGTTT CACTGAAAAC TTCAGGCGAC CTTTGCGGCA AACTCAAAAC	3240
CACCCTTAAA ACCTTGGTCT GCTCTTTGGT TTCCCTGAGT ATGGTATTGC CTGCCCATGC	3300
CCAAATTACC ACCGACAAAT CAGCACCTAA AAACCAGCAG GTCGTTATCC TTAAAACCAA	3360
CACTGGTGCC CCCTTGGTGA ATATCCAAAC TCCGAATGGA CGCGGATTGA GCCACAACCG	3420
CTATACGCAG TTTGATGTTG ACAACAAAGG GGCAGTGTTA AACAACGACC GTAACAATAA	3480
TCCGTTTCTG GTCAAAGGCA GTGCGCAATT GATTTTGAAC GAGGTACGCG GTACGGCTAG	3540
CAAACCTAAC GGCATCGTTA CCGTAGGCGG TCAAAGGCC GACGTGATTA TTGCCAACCC	3600
CAACGGCATT ACCGTTAATG GCGGCGGCTT TAAAAATGTC GGTCGGGGCA TCTTAACAT	3660
CGGTGCGCCC CAAATCGGCA AAGACGGTGC ACTGACAGGA TTTGATGTGC GTCAAGGCAC	3720
ATTGACCGTA GGAGCAGCAG GTTGGAATGA TAAAGGCGGA GCCGACTACA CCGGGGTACT	3780

0928457.081401

TGCTCGTGCA GTTGCTTTGC AGGGGAAATT ACAGGGTAAA AACCTGGCGG TTTCTACCGG	3840
TCCTCAGAAA GTAGATTACG CCAGCGGCGA AATCAGTGCA GGTACGGCAG CGGGTACGAA	3900
ACCGACTATT GCCCTTGATA CTGCCGCACT GGGCGGTATG TACGCCGACA GCATCACACT	3960
GATTGCCAAT GAAAAAGGCG TAGGCGTCAA AAATGCCGGC AACTCGAAG CGGCCAAGCA	4020
ATTGATTGTG ACTTCGTCAG GCCGCATTGA AAACAGCGGC CGCATCGCCA CCACTGCCGA	4080
CGGCACCGAA GCTTCACCGA CTTATCTCTC CATCGAAACC ACCGAAAAAG GAGCGGCAGG	4140
CACATTTATC TCCAATGGTG GTCGGATCGA GAGCAAAGGC TTATTGGTTA TTGAGACGGG	4200
AGAAGATATC AGCTTGCGTA ACGGAGCCGT GGTGCAGAAT AACGGCAGTC GCCCAGCTAC	4260
CACGGTATTA AATGCTGGTC ATAATTTGGT GATTGAGAGT AAAACTAATG TGAACAATGC	4320
CAAAGGCTCG GCTAATCTGT CGGCCGGCGG TCGTACTACG ATCAATGATG CTACTATTCA	4380
AGCGGGCAGT TCCGTGTACA GCTCCACCAA AGGCGATACT GAATTGGGTG AAAATACCCG	4440
TATTATTGCT GAAAACGTAA CCGTATTATC TAACGGTAGT ATTGGCAGTG CTGCTGTAAT	4500
TGAGGCTAAA GAACTGCAC ACATTGAATC GGGCAAACCG CTTTCTTTAG AAACCTCGAC	4560
CGTTGCCTCC AACATCCGTT TGAACAACGG TAACATTAAA GGCGGAAAGC AGCTTGCTTT	4620
ACTGGCAGAC GATAACATTA CTGCCAAAAC TACCAATCTG AATACTCCCG GCAATCTGTA	4680
TGTTCATACA GGTAAAGATC TGAATTTGAA TGTGATAAA GATTTGTCTG CCGCCAGCAT	4740
CCATTTGAAA TCGGATAACG CTGCCCATAT TACCGGCACC AGTAAAACCC TCACTGCCTC	4800
AAAAGACATG GGTGTGGAGG CAGGCTTGCT GAATGTTACC AATACCAATC TCGGTACCAA	4860
CTCGGGTAAT CTGCACATTC AGGCAGCCAA AGGCAATATT CAGCTTCGCA ATACCAAGCT	4920

F04T50-2542650

GAACGCAGCC AAGGCTCTCG AAACCACCGC ATTGCAGGGC AATATCGTTT CAGACGGCCT	4980
TCATGCTGTT TCTGCAGACG GTCATGTATC CTTATTGGCC AACGGTAATG CCGACTTTAC	5040
CGGTCACAAT ACCCTGACAG CCAAGGCCGA TGTCAATGCA GGATCGGTTG GTAAAGGCCG	5100
TCTGAAAGCA GACAATACCA ATATCACTTC ATCTTCAGGA GATATTACGT TGGTTGCCGG	5160
CAACGGTATT CAGCTTGGTG ACGGAAAACA ACGCAATTCA ATCAACGGAA AACACATCAG	5220
CATCAAAAAC AACGGTGGTA ATGCCGACTT AAAAAACCTT AACGTCCATG CCAAAGCGG	5280
GGCATTGAAC ATTCATTCCG ACCGGGCATT GAGCATAGAA AATACCAAGC TGGAGTCTAC	5340
CCATAATACG CATCTTAATG CACAACACGA GCGGGTAACG CTCAACCAAG TAGATGCCTA	5400
CGCACACCGT CATCTAAGCA TTACCGGCAG CCAGATTTGG CAAAACGACA AACTGCCTTC	5460
TGCCAACAAG CTGGTGGCTA ACGGTGTATT GGCCTCAAT GCGCGCTATT CCCAAATTGC	5520
CGACAACACC ACGCTGAGAG CGGGTGCAAT CAACCTTACT GCCGGTACCG CCCTAGTCAA	5580
GCGCGGCAAC ATCAATTGGA GTACCGTTTC GACCAAGACT TTGGAAGATA ATGCCGAATT	5640
AAAACCATTG GCCGGACGGC TGAATATTGA AGCAGGTAGC GGCACATTAA CCATCGAACC	5700
TGCCAACCGC ATCAGTGCGC ATACCGACCT GAGCATCAAA ACAGGCGGAA AATTGCTGTT	5760
GTCTGCAAAA GGAGGAAATG CAGGTGCGCC TAGTGCTCAA GTTTCCTCAT TGGAAGCAAA	5820
AGGCAATATC CGTCTGGTTA CAGGAGAAAC AGATTTAAGA GGTTCTAAAA TTACAGCCGG	5880
TAAAACTTG GTTGTCGCCA CCACCAAAGG CAAGTTGAAT ATCGAAGCCG TAAACAATC	5940
ATTCAGCAAT TATTTTCCTA CACAAAAAGC GGCTGAACTC AACCAAAAAT CCAAAGAATT	6000

104180 257 0928457

GGAACAGCAG ATTGCGCAGT TGAAAAAAG CTCGCCTAAA AGCAAGCTGA TTCCAACCCT	6060
GCAAGAAGAA CGCGACCGTC TCGCTTTCTA TATTCAAGCC ATCAACAAGG AAGTTAAAGG	6120
TAAAAAACC AAAGGCAAAG AATACCTGCA AGCCAAGCTT TCTGCACAAA ATATTGACTT	6180
GATTTCCGCA CAAGGCATCG AAATCAGCGG TTCCGATATT ACCGCTTCCA AAAAAGTAA	6240
CCTTCACGCC GCAGGCGTAT TGCCAAAGGC AGCAGATTCA GAGGCGGCTG CTATTCTGAT	6300
TGACGGCATA ACCGACCAAT ATGAAATTGG CAAGCCCACC TACAAGAGTC ACTACGACAA	6360
AGCTGCTCTG AACAAGCCTT CACGTTTGAC CGGACGTACG GGGGTAAGTA TTCATGCAGC	6420
TGCGGCACTC GATGATGCAC GTATTATTAT CGGTGCATCC GAAATCAAAG CTCCCTCAGG	6480
CAGCATAGAC ATCAAAGCCC ATAGTGATAT TGTACTGGAG GCTGGACAAA ACGATGCCTA	6540
TACCTTCTTA AAAACCAAAG GTAAAAGCGG CAAAATCATC AGAAAAACCA AGTTTACCAG	6600
CACCCGCGAC CACCTGATTA TGCCAGCCCC CGTCGAGCTG ACCGCCAAG GTATCAGCT	6660
TCAGGCAGGC GGCAACATCG AAGCTAATAC CACCCGCTTC AATGCCCCTG CAGGTAAAGT	6720
TACCCTGGTT GCGGGTGAAG AGCTGCAACT GCTGGCAGAA GAAGGCATCC ACAAGCACGA	6780
GTTGGATGTC CAAAAAGCC GCCGCTTTAT CGGCATCAAG GTAGGTAAGA GCAATTACAG	6840
TAAAAACGAA CTGAACGAAA CCAAATTGCC TGTCCGCGTC GTCGCCCAA CTGCAGCCAC	6900
CCGTTCAGGC TGGGATACCG TGCTCGAAGG TACCGAATTC AAAACCACGC TGGCCGGTGC	6960
CGACATTAG GCAGGTGTAG GCGAAAAAGC CCGTGTGAT GCGAAAATTA TCCTCAAAGG	7020
CATTGTGAAC CGTATCCAGT CGGAAGAAAA ATTAGAAACC AACTCAACCG TATGGCAGAA	7080
ACAGGCCGGA CGCGGCAGCA CTATCGAAAC GCTAAAGTCC CCCAGCTTCG AAAGCCCTAC	7140

09020457.081401

TCCGCCCAA	TTGTCCGCAC	CCGGCGGCTA	TATCGTCGAC	ATTCCGAAAG	GCAATCTGAA	7200
AACCGAAATC	GAAAAGCTGT	CCAAACAGCC	CGAGTATGCC	TATCTGAAAC	AGCTCCAAGT	7260
AGCGAAAAAC	ATCAACTGGA	ATCAGGTGCA	GCTTGCTTAC	GACAGATGGG	ACTACAAACA	7320
GGAGGGCTTA	ACCGAAGCAG	GTGCGGCGAT	TATCGCACTG	GCCGTTACCG	TGGTCACCTC	7380
AGGCGCAGGA	ACCGGAGCCG	TATTGGGATT	AAACGGTGCG	GCCGCCGCCG	CAACCGATGC	7440
AGCATTGCC	TCTTTGGCCA	GCCAGGCTTC	CGTATCGTTC	ATCAACAACA	AAGGCGATGT	7500
CGGCAAAACC	CTGAAAGAGC	TGGGCAGAAG	CAGCACGGTG	AAAATCTGG	TGGTTGCCGC	7560
CGCTACCGCA	GGCGTAGCCG	ACAAAATCGG	CGCTTCGGCA	CTGAACAATG	TCAGCGATAA	7620
GCAGTGGATC	AACAACCTGA	CCGTCAACCT	AGCCAATGCG	GGCAGTGCCG	CACTGATTAA	7680
TACCGCTGTC	AACGGCGGCA	GCCTGAAAGA	CAATCTGGAA	GCGAATATCC	TTGCGGCTTT	7740
GGTCAATACC	GCGCATGGAG	AAGCAGCCAG	TAAAATCAAA	CAGTTGGATC	AGCACTACAT	7800
AGTCCACAAG	ATTGCCCATG	CCATAGCGGG	CTGTGCGGCA	GCGGCGGCGA	ATAAGGGCAA	7860
GTGTCAGGAT	GGTGCGATAG	GTGCGGCTGT	GGGCGAGATA	GTCGGGGAGG	CTTTGACAAA	7920
CGGCAAAAAT	CCTGACACTT	TGACAGCTAA	AGAACGCGAA	CAGATTTTGG	CATACAGCAA	7980
ACTGGTTGCC	GGTACGGTAA	GCGGTGTGGT	CGGCGGCGAT	GTAAATGCGG	CGGCGAATGC	8040
GGCTGAGGTA	GCGGTGAAAA	ATAATCAGCT	TAGCGACAAA	GAGGGTAGAG	AATTTGATAA	8100
CGAAATGACT	GCATGCGCCA	AACAGAATAA	TCCTCAACTG	TGCAGAAAAA	ATACTGTAAA	8160
AAAGTATCAA	AATGTTGCTG	ATAAAAGACT	TGCTGCTTCG	ATTGCAATAT	GTACGGATAT	8220

09928457.081401

ATCCCGTAGT ACTGAATGTA GAACAATCAG AAAACAACAT TTGATCGATA GTAGAAGCCT	8280
TCATTCATCT TGGGAAGCAG GTCTAATTGG TAAAGATGAT GAATGGTATA AATTATTCAG	8340
CAAATCTTAC ACCCAAGCAG ATTTGGCTTT ACAGTCTTAT CATTTGAATA CTGCTGCTAA	8400
ATCTTGGCTT CAATCGGGCA ATACAAAGCC TTTATCCGAA TGGATGTCCG ACCAAGGTTA	8460
TACACTTATT TCAGGAGTTA ATCCTAGATT CATTCOAATA CCAAGAGGGT TTGTAAAACA	8520
AAATACACCT ATTACTAATG TCAAATACCC GGAAGGCATC AGTTTCGATA CAAACCTAAA	8580
AAGACATCTG GCAAATGCTG ATGGTTTTAG TCAAGAACAG GGCATTAAAG GAGCCCATAA	8640
CCGCACCAAT TTTATGGCAG AACTAAATTC ACGAGGAGGA CGCGTAAAAT CTGAAACCCA	8700
AACTGATATT GAAGGCATTA CCCGAATTAA ATATGAGATT CCTACACTAG ACAGGACAGG	8760
TAAACCTGAT GGTGGATTTA AGGAAATTTT AAGTATAAAA ACTGTTTATA ATCCTAAAAA	8820
ATTTTCTGAT GATAAAATAC TTCAAATGGC TCAAATGCT GCTTCACAAG GATATTCAAA	8880
AGCCTCTAAA ATTGCTCAAA ATGAAAGAAC TAAATCAATA TCGGAAAGAA AAAATGTCAT	8940
TCAATTCTCA GAAACCTTTG ACGGAATCAA ATTTAGATCA TATTTTGATG TAAATACAGG	9000
AAGAATTACA AACATTCACC CAGAATAATT TAAAGGAAAA ATTATGAAAA ATAATATTTT	9060
TCTAAACTTA AATAAAAAAT CTATAAATAA CAACCATTTT GTTATTTTGA TTTTTTTGA	9120
AACAATTTAC CAATTTGAAA CTAAAGATAC GCTTTTAGAG TGTTTTAAAA ATATTACAAC	9180
TACCGGACAT TTTGGAGTAA TAGGTGCTCA ATATGAAAAA ATAGATGCTA CCAGATGGAT	9240
TGGAGATTAT GAAGAGGTAA ATGGATTTGA GTATATTGAT AAAGCTCCTT CTATTTATTT	9300
TTCAAGTTGA GATGATTTCA ATCCTGAAGA ATTAATTATA CCTATTAATT TAGCATATCA	9360

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TTACTTTAAT ATTGCAATAT CTGATTTCTT AATAGCTCAC CCTGAATATC AAAAAAAGTG	9420
TAAAGAAATA CAAAAACAT ATTCTCAAAC AACTGTAGC CTGCATGAAA CCTAAAATCC	9480
ATGCGTAAGG TGTGTGCTTC AGCACGCACG CGTTCCATGA TTTACGGCTC AATGCCGTCT	9540
GAAAAGCTCA CAATTTTTC A GACGGCATTT GTTATGCAAG TAAATATTCA GATTCCCTAT	9600
ATACTGCCCA GACGCGTGCG TGCTGAAGAC ACCCCCTACG CTTGCTGCAG AACTTTTCGGG	9660
TAAAACCGGT GTGAGCATT A GCGCACCGTA TGCCAATGAG AACAGTCGCA TCCTGCTCAG	9720
CACCACGGAT ATCAGTTCGG AAAACGGCAA AATCAAAATT CAATCTTACG GTGACCAATA	9780
TTACTATGCG AGACAGAGCG AACTCTATAC CTTTGAACGC CGCAGCTACA AACTTGGCAA	9840
ATGGTACAAC CGCAAACACA TTACCGAAGT CAAAGAACAC AAAAAACGCCA AGCCCGACGC	9900
AGTAAACCTC AGCGCATCCC AAGGCATCGA CATCAAATCT GGTGGCAGCA TCGACGCCTA	9960
CGCCACCGCA TTCGATGCCC CCAAAGGCAG CATTAAACATC GAAGCCGGGC GGAAATTGAC	10020
ACTCTATGCC GTAGAAGAGC TCAACTACGA CAACTAGAC AGCCAAAAAA GGCGCAGATT	10080
TCTCGGCATC AGCTACAGCA AAGCACACGA CACCACCACC CAAGTCATGA AAACCGCGCT	10140
GCCCTCAAGG GTAGTTGCAG AATCAGCCAA CCTCCAATCG GGCTGGGATA CCAAAGTGCA	10200
AGGCACACAG TTTGAAACCA CACTGGGTGG CGCAACCATA CGCGCAGGCG TAGGTGAGCA	10260
GGCACGGGCA GATGCCAAGA TTATCCTCGA AGGGATCAAA AGCAGCATCC ACACAGAAAC	10320
CGTGAGCAGC AGCAAATCTA CTCTATGGCA AAAACAGGCA GGACGGGGCA GTAACATCGA	10380
AACCTTGCAA TTGCCGAGTT TCACCGGTCC CGTTGCGCCC GTACTGTCCG CACCCGGCGG	10440

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TTACATTGTC GACATTCCGA AAGGCAATCT GAAAACCCAA ATCGAAACCC TCACCAAGCA	10500
GCCCGAGTAT GCTTATTTGA AACAACTTCA AGTTGCGAAA AACATCAACT GGAATCAGGT	10560
GCAGCTTGCT TACGATAAAT GGGACTACAA ACAGGAGGGC ATGACACCCG CAGCAGCAGC	10620
TGTCGTCGTT ATCGTCGTAA CCGTATTGAC CTACGGTGCA CTGTCCGCCC CGGCAGCCGC	10680
CGGAACGGCG GCGCGGGCAG GCGCAGGAGC GGGAGGAGCC GCAGCAGGAA CGGCAGCCGG	10740
AACTGGAGTA GCAGCAGGAA CGGCAGCCAC AACCGGAGTA GCAGCAGGCA CATCAGCTGC	10800
AGCTATCACC ACAGCCGCAG GCAAAGCCGC ACTGGCCAGT CTCGCCAGCC AAGCCGCAGT	10860
TTCCCTCATC AACACAAAG GAGACATAAA CCATACCCTG AAAGAACTGG GCAAAGCAG	10920
CACCGTCAGA CAGGCCGCCA CCGCCGCCGT AACCGCAGGC GTACTGCAGG GCATAAGCGG	10980
GCTGAACACC CAAGCAGCCG AAGCCGTCAG CAAACATTTT CACAGTCCCG CAGCAGGCAA	11040
ACTGACCGCT AACCTGATCA ACAGCACCGC TGCCGCAAGT GTCCATACCG CCATCAACGG	11100
CGGCAGCCTG AAAGACAACT TGGGCGATGC CGCACTGGGT GCGATAGTCA GTACCGTACA	11160
CGGAGAAGTA GCGAGCAAAA TCAAATTTAA TCTCAGCGAA GACTACATTG CCCACAAGAT	11220
AGCCCATGCC GTAGCAGGCT GTGCATCGGC GGTAGCAAAT AAAGGCAAAT GTCGGGACGG	11280
CGCAATCGGC GCGGCAGTCG GCGAGATGGT GGGAGAAACC CTGTTGGACG GACGCGATGT	11340
AGGCAAACCTG TCACCCCAAG AACGCCAAAA AGTCATAGCC TACTCGCAGA TTATCGCAGG	11400
CAGCGCAGTG GCATTGGTTA AAGGGGATGT GAATACGGCG GTGAATGCGG CTA CTGTGGC	11460
AGTGGAGAAT AATAGTCTTT TAGCTCGCAG GAGGGTAAAT ATACGTTGGA CTCCGCGACA	11520
AGAATTGGAA CATGAATATG CCATTCTTGA AATCCAGGCC ATTACCAATC AAATCCGAAG	11580

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GCTGGATCCG	AAATTTAACG	GGATTGCTAT	TCTGAGGACT	CCTGGAGAGC	CGTGGACAAG	11640
ACATGATGTA	CAAACATACA	GGCAATATTA	TAATCAATTA	AGGGAATCCA	GAGGCTTTGC	11700
TGTTGAACCA	ATTTATAGAA	TCAGGATAAA	CAACGGCAAT	GAATTTAACC	GTATCATGTC	11760
ATCAAAATAC	CCTTATAATG	AGCTTTATGT	AGCCAATCCT	AAATCGGCGA	CGGGGTATTT	11820
TAGGGTAGAT	TCGTATGATC	CTGCGACAAG	GGAAATTATT	TCAAGAAAAT	TTACCCAATT	11880
TTCTCAAATC	CAAGAAAGTA	CGGGGATTGG	TTATATCAAG	GAGGCTGTTA	GAAAAATATAG	11940
CCCTGGTACT	GTCATTTCCA	ATGTTCCAAG	TACACCTACT	ACGATAAGAG	GAAGAAAAGCT	12000
TGAAGGAAAA	CTTATTTTAG	AAGTTCCTGC	TCAGGTCAAT	CCAATTCCAC	AATCTGTATT	12060
AAGGGCGGCA	CAAGAAGAAA	ATGTTATCAT	TAGAGATACA	ACAGGAAGGA	TTTACAAATG	12120
AAGAAAGATA	TTTTTTATTG	TGAGCAGTGG	TCTTATGGTT	ATAAGAGACT	TCATAAGCCT	12180
TTTTCTGAGA	AACAAGCTGA	GGAAAAACAT	CTTAAAGGGG	AGTTATATAC	TGCCGTAATA	12240
GGTTCGGCGA	CACAACCTGA	ATATGTAATT	ACCTTGCGAG	AGGAAGTAGG	TTTTTTTTTCG	12300
GTAAATTTTT	TCGATAAATT	TGGAAGGGAT	TATTTAACCC	ATCAATTTCA	AAAATATTCC	12360
AATTCGAATT	ATTATTTTCT	TTCTATGGCT	GTATGGAGAG	ATTATATAAC	TTTGGAAATCT	12420
CATGACTTAG	CAGAAGGATA	TACTTATTTT	TTCAATGAAA	ATACGGATGA	TTGCTATGTT	12480
TTGAAACAAG	ATTTTATTAA	TAATGAGCGA	TATGAAAAAA	CAGAATTATA	TTCCCAAAAA	12540
GATAAGGTAA	TTCTATTTCC	AAAGTTTGGT	GAATATGATT	TGGTGTTAAA	TCCGGACATT	12600
ATTTAATTAA	GTTTTAAGGC	CGTCTGAAAA	AAATTTCAAA	CGGCTTTTAT	TATTGGGTTT	12660

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GGAATCTGAG GATAAAGCTG ATAAAAACCA GGAAATTATC AGATTGCTAT ATACGTATTG	12720
TTGTACAGAC TAAAGGCAGC AATCAAATCA CTATTGCTTA CCCACAAAAA TAAATTGATT	12780
ATATGGAATA ATCATGAATA AGAGAATGAA AATGTGTCCT GCTTGTCAAC AAGGCTATCT	12840
CTACCATTCTG AAACCTAAAT ATCTTCATGA TGAAATTATT CTGTGTGATG AATGCGATGC	12900
AGTATGGCTC AAAGGTATGA ATATATTTTA TGGAGAATAT GAAAAAGATT TTTATTCTTA	12960
TGTTCCTTTC ATGGAATCCC AAGGTATAAC GAGTGAATGT ATTGGGAAG GAGATTGT	13020
TGATCATCCA TATTATGAAG ATGAAAACTC AAATGATATG GATTGATGGA AATTTTAAGC	13080
CTGCGTAGGT ACGATTAGCC ATCAAACGGC GTAATCATAC GCAAGATTAT CAACAGAGAG	13140
GGCTGGCAGC GATATACCAC CCACAAGATT GCCCATGCCA TAGCGGGCTG TCGGCAGCG	13200
GCGGCGAATA AGGGCAAGTG TCAGGATGGT GCGATAGGCG CTGCAGTCGG TGAGATTGT	13260
GGTGAGGCTT TGGTTAAGAA TACTGATTTT AGTCGTATGA GTGCGACCGA AATCGAAAAA	13320
GCTAAAGCGA AGATTACTGC CTATTCAAAA CTGGTTGCCG GCACTGCGTC TGCCGTTGTA	13380
GGCGGGGATG TGAATACAGC GGCGAATGCG GCACAGATAG CCGTGAGAA TAATACTTTG	13440
TATCCTAGAT GCGTTGGTGC AAAGTGTGAT GAATTTCAAA AGGAACAACA AAAATGGATA	13500
CGTGAAAATC CTGAAGAATA TCGAGAAGTT TTGCTTTTTT AGACAGGATT TATTCCAATT	13560
ATCGGTGATA TACAGAGTTT TGTACAAGCA CAGACCGCTG CCGATCACCT GTTTGCTTTG	13620
CTGGGTGTGG TTCCGGGTAT CGGTGAATCG ATACAGGCCT ATAAAGTAGC GAAAGCGGCA	13680
AAAAATTTAC AAGGCATGAA AAAAGCCTTG GACAAGGCAG CAACCGTTGC CACTGCACAG	13740
GGCTATGTCA GCAAAACCAA AATCAAATC GGTCAAATG AATTAAGGGT TACTGCAGCA	13800

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ACTGACAAAC AATTGCTGAA AGCTATTGGC GAAGGAAGGG ACACGACAGG TAAAATGACC	13860
GAGCAGTTAT TTGACTCTTT AGCTAAACAA AATGGCTTCA GAGTGCTTTC GGGCGGCAAA	13920
TACGGCGGAA ATAACGGTTT TGATCATGTA TGGCAGGCTG CCGATGGTAG TGTCGTTTTG	13980
ATTGTAGAAA GTAAGCAGAT TAGGAACGGT ACGGTACAGC TGAATCCGAA TGGTGCGGGT	14040
GGATATACGC AAATGAGTGA GGATTGGATT AGACAAGTTT TAGATCAATT ACCCGATGGT	14100
AGTCCCCTA AAGCTGCTGT CTTCAAAGCA AATAAGAACG GCACATTAAA AACAGCAATA	14160
GCAGGCGTTG ATCGTCAAAC AGGTAAGGCC GTTATTCTTC CTGTCAAAGT TCCTTCTAAA	14220
ACCAATATAA GGAGATAACA ATGGGGCACA ATATGATGAC CACCCAAAAA TGGTATGAGC	14280
ATATTACTAA TGTAATCATA GGCAATACTG CTAATTTCAA TAGCGGTTGC CTTGACTCTA	14340
TAGATTATGT AGATGAAAGA AAAGGCGTTC CGCTTGCAGC TATGCAACAT ATTTTCATGG	14400
ACGTTAGAGC TGCAGCTTCC CATGCCTATC TATTTGAACA TGATCTTAAG AAATTCAAGC	14460
AATATGCTTA TGTTGCAGGA AAGCTGGGGG TTTTGCTGAG TGTAAATTCT ACAGACCCTG	14520
AACCCTTCTT CTTTCCCTGT GACATGCTCA ACATTCAAAA TCCGATGTTT CTGATGCTGA	14580
TGAGCGACAG CCCACAGCTG CGTGAGTTTC TGGTGCGCAA TATCGACAAC ATCGCCAACG	14640
ATACAGAAGC CTTTATAAAC CGCTACGACC TCAACCGGCA TATGATTTAC AATACTCTGC	14700
TGATGGTGGA GGGTAAGCAG CTTGATCGGT TGAAACAACG TAGCGAGAAA GTCTTGGCGC	14760
ATCCCACCCC TAGCAAATGG CTGCAAAAGC GGTGTACGA TTACCGCTTC TTCCTCGCTT	14820
TCGCCGAACA GGATGCCGAG GCAATGAAAG CCGCCTTAGA GCCGCTTTTC GATAAAAAAA	14880

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CCGCGCGTAT GGCTGCCAAA GAAACATTGT CCTATTTCTGA TTTCTACCTG CAGCCGCAAA 14940

TCGTTACCTA CGCCAAAATC GCATCCATGC ACGGTTTCTGA TTTGGGCATA GATCAAGAAA 15000

TCTCACCGAG GGATTTGATT GTTTACGATC CGCTGCCGGC AGACGAATAT CAAGACATCT 15060

TCGATTTTAT GAAACAGTAT GACTTGTCTT ACCCGTATGA ATATCTGCAG GATTGGATAG 15120

ATTACTATAC GTTCAAAACC GATAAGCTGG TATTTGGTAA CGCGAAGCGA GAGTGAGCCG 15180

TAAAACTCTG AGCTCCTGTT TTATAGATTA CAACTTTAGG CCGTCTTAAA GCTGAAAGAT 15240

TTTCGAAAGC TATAAATTGA AGCCCTTCCA CAGTACATAG ATCTGTGTTG TGGCGGGGCT 15300

TTACCACGCT GATTGCCGGA GAAGAACTCA ACCTGCTGGC AAAACAAGGC ATGAGATCTT 15360

TGCAATAACA TGAGTTGAGA CCTTTGCAAA AAAGCCCTTC CCCGACATCC GAAACCCAAA 15420

CACAGGATTT CGGCTGTTTT CGTACCAAAT ACCTCCTAAT TTTACCCAAA TACCCCCTTA 15480

ATCCTCCTCG GACACCCGAT AATCAGGCAT CCGGGCTGCC TTTTAGGCGG CAGCGGGCGC 15540

ATTTAGCCTG TTGGCCGCTT TCAACAGGTT CAAACACATC GCCTTCAGGT GGCTTTGCGC 15600

ACTCACTTTG TCATTTCCAA 15620

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 acides aminés
- (B) TYPE : acide aminé
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: peptide

09926457.001401

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION:1..580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Met Lys Phe Phe Pro Ala Pro Cys Leu Leu Val Ile Leu Ala Val Ile
1 5 10 15

Pro Leu Lys Thr Leu Ala Ala Asp Glu Asn Asp Ala Glu Leu Ile Arg
20 25 30

Ser Met Gln Arg Gln Gln His Ile Asp Ala Glu Leu Leu Thr Asp Ala
35 40 45

Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser
50 55 60

Glu Asp Glu Thr Pro Cys Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp
65 70 75 80

Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu
85 90 95

Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg
100 105 110

Leu Gln Lys Ala Ala Gln Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr
115 120 125

Ser Gln Ala Ile Ile Gln Pro Gln Asn Met Asp Ser Gly Ile Leu Lys
130 135 140

Leu Arg Val Ser Ala Gly Glu Ile Gly Asp Ile Arg Tyr Glu Glu Lys
145 150 155 160

Arg Asp Gly Lys Ser Ala Glu Gly Ser Ile Ser Ala Phe Asn Asn Lys

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	165		170		175										
Phe	Pro	Leu	Tyr	Arg	Asn	Lys	Ile	Leu	Asn	Leu	Arg	Asp	Val	Glu	Gln
	180				185								190		
Gly	Leu	Glu	Asn	Leu	Arg	Arg	Leu	Pro	Ser	Val	Lys	Thr	Asp	Ile	Gln
	195						200						205		
Ile	Ile	Pro	Ser	Glu	Glu	Glu	Gly	Lys	Ser	Asp	Leu	Gln	Ile	Lys	Trp
	210						215						220		
Gln	Gln	Asn	Lys	Pro	Ile	Arg	Phe	Ser	Ile	Gly	Ile	Asp	Asp	Ala	Gly
225				230						235				240	
Gly	Lys	Thr	Thr	Gly	Lys	Tyr	Gln	Gly	Asn	Val	Ala	Leu	Ser	Phe	Asp
				245					250					255	
Asn	Pro	Leu	Gly	Leu	Ser	Asp	Leu	Phe	Tyr	Val	Ser	Tyr	Gly	Arg	Gly
		260						265						270	
Leu	Val	His	Lys	Thr	Asp	Leu	Thr	Asp	Ala	Thr	Gly	Thr	Glu	Thr	Glu
		275					280						285		
Ser	Gly	Ser	Arg	Ser	Tyr	Ser	Val	His	Tyr	Ser	Val	Pro	Val	Lys	Lys
	290					295						300			
Trp	Leu	Phe	Ser	Phe	Asn	His	Asn	Gly	His	Arg	Tyr	His	Glu	Ala	Thr
305					310					315				320	
Glu	Gly	Tyr	Ser	Val	Asn	Tyr	Asp	Tyr	Asn	Gly	Lys	Gln	Tyr	Gln	Ser
				325					330					335	
Ser	Leu	Ala	Ala	Glu	Arg	Met	Leu	Trp	Arg	Asn	Arg	Phe	His	Lys	Thr
		340						345					350		
Ser	Val	Gly	Met	Lys	Leu	Trp	Thr	Arg	Gln	Thr	Tyr	Lys	Tyr	Ile	Asp

09920457-001401

355	360	365
Asp Ala Glu Ile Glu Val Gln Arg Arg Arg Ser Ala Gly Trp Glu Ala		
370	375	380
Glu Leu Arg His Arg Ala Tyr Leu Asn Arg Trp Gln Leu Asp Gly Lys		
385	390	395 400
Leu Ser Tyr Lys Arg Gly Thr Gly Met Arg Gln Ser Met Pro Ala Pro		
405	410	415
Glu Glu Asn Gly Gly Gly Thr Ile Pro Gly Thr Ser Arg Met Lys Ile		
420	425	430
Ile Thr Ala Gly Leu Asp Ala Ala Ala Pro Phe Met Leu Gly Lys Gln		
435	440	445
Gln Phe Phe Tyr Ala Thr Ala Ile Gln Ala Gln Trp Asn Lys Thr Pro		
450	455	460
Leu Val Ala Gln Asp Lys Leu Ser Ile Gly Ser Arg Tyr Thr Val Arg		
465	470	475 480
Gly Phe Asp Gly Glu Gln Ser Leu Phe Gly Glu Arg Gly Phe Tyr Trp		
485	490	495
Gln Asn Thr Leu Thr Trp Tyr Phe His Pro Asn His Gln Phe Tyr Leu		
500	505	510
Gly Ala Asp Tyr Gly Arg Val Ser Gly Glu Ser Ala Gln Tyr Val Ser		
515	520	525
Gly Lys Gln Leu Met Gly Ala Val Val Gly Phe Arg Gly Gly His Lys		
530	535	540
Val Gly Gly Met Phe Ala Tyr Asp Leu Phe Ala Gly Lys Pro Leu His		
545	550	555 560

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 104180-25482660

Lys Pro Lys Gly Phe Gln Thr Thr Asn Thr Val Tyr Gly Phe Asn Leu
 565 570 575

Asn Tyr Ser Phe
 580

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1981 acides aminés
- (B) TYPE : acide aminé
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1..1981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Met Asn Lys Gly Leu His Arg Ile Ile Phe Ser Lys Lys His Ser Thr
 1 5 10 15

Met Val Ala Val Ala Glu Thr Ala Asn Ser Gln Gly Lys Gly Lys Gln
 20 25 30

Ala Gly Ser Ser Val Ser Val Ser Leu Lys Thr Ser Gly Asp Leu Cys
 35 40 45

Gly Lys Leu Lys Thr Thr Leu Lys Thr Leu Val Cys Ser Leu Val Ser
 50 55 60

Leu Ser Met Val Leu Pro Ala His Ala Gln Ile Thr Thr Asp Lys S r

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 104780/25482660

65	70	75	80
Ala Pro Lys Asn Gln Gln Val Val Ile Leu Lys Thr Asn Thr Gly Ala			
	85	90	95
Pro Leu Val Asn Ile Gln Thr Pro Asn Gly Arg Gly Leu Ser His Asn			
	100	105	110
Arg Tyr Thr Gln Phe Asp Val Asp Asn Lys Gly Ala Val Leu Asn Asn			
	115	120	125
Asp Arg Asn Asn Asn Pro Phe Leu Val Lys Gly Ser Ala Gln Leu Ile			
	130	135	140
Leu Asn Glu Val Arg Gly Thr Ala Ser Lys Leu Asn Gly Ile Val Thr			
	145	150	155
Val Gly Gly Gln Lys Ala Asp Val Ile Ile Ala Asn Pro Asn Gly Ile			
	165	170	175
Thr Val Asn Gly Gly Gly Phe Lys Asn Val Gly Arg Gly Ile Leu Thr			
	180	185	190
Ile Gly Ala Pro Gln Ile Gly Lys Asp Gly Ala Leu Thr Gly Phe Asp			
	195	200	205
Val Arg Gln Gly Thr Leu Thr Val Gly Ala Ala Gly Trp Asn Asp Lys			
	210	215	220
Gly Gly Ala Asp Tyr Thr Gly Val Leu Ala Arg Ala Val Ala Leu Gln			
	225	230	235
Gly Lys Leu Gln Gly Lys Asn Leu Ala Val Ser Thr Gly Pro Gln Lys			
	245	250	255
Val Asp Tyr Ala Ser Gly Glu Ile Ser Ala Gly Thr Ala Ala Gly Thr			
	260	265	270

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Lys Pro Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met Tyr Ala
275 280 285

Asp Ser Ile Thr Leu Ile Ala Asn Glu Lys Gly Val Gly Val Lys Asn
290 295 300

Ala Gly Thr Leu Glu Ala Ala Lys Gln Leu Ile Val Thr Ser Ser Gly
305 310 315 320

Arg Ile Glu Asn Ser Gly Arg Ile Ala Thr Thr Ala Asp Gly Thr Glu
325 330 335

Ala Ser Pro Thr Tyr Leu Ser Ile Glu Thr Thr Glu Lys Gly Ala Ala
340 345 350

Gly Thr Phe Ile Ser Asn Gly Gly Arg Ile Glu Ser Lys Gly Leu Leu
355 360 365

Val Ile Glu Thr Gly Glu Asp Ile Ser Leu Arg Asn Gly Ala Val Val
370 375 380

Gln Asn Asn Gly Ser Arg Pro Ala Thr Thr Val Leu Asn Ala Gly His
385 390 395 400

Asn Leu Val Ile Glu Ser Lys Thr Asn Val Asn Asn Ala Lys Gly Ser
405 410 415

Ala Asn Leu Ser Ala Gly Gly Arg Thr Thr Ile Asn Asp Ala Thr Ile
420 425 430

Gln Ala Gly Ser Ser Val Tyr Ser Ser Thr Lys Gly Asp Thr Glu Leu
435 440 445

Gly Glu Asn Thr Arg Ile Ile Ala Glu Asn Val Thr Val Leu Ser Asn
450 455 460

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Gly Ser Ile Gly Ser Ala Ala Val Ile Glu Ala Lys Asp Thr Ala His
465 470 475 480

Ile Glu Ser Gly Lys Pro Leu Ser Leu Glu Thr Ser Thr Val Ala Ser
485 490 495

Asn Ile Arg Leu Asn Asn Gly Asn Ile Lys Gly Gly Lys Gln Leu Ala
500 505 510

Leu Leu Ala Asp Asp Asn Ile Thr Ala Lys Thr Thr Asn Leu Asn Thr
515 520 525

Pro Gly Asn Leu Tyr Val His Thr Gly Lys Asp Leu Asn Leu Asn Val
530 535 540

Asp Lys Asp Leu Ser Ala Ala Ser Ile His Leu Lys Ser Asp Asn Ala
545 550 555 560

Ala His Ile Thr Gly Thr Ser Lys Thr Leu Thr Ala Ser Lys Asp Met
565 570 575

Gly Val Glu Ala Gly Leu Leu Asn Val Thr Asn Thr Asn Leu Arg Thr
580 585 590

Asn Ser Gly Asn Leu His Ile Gln Ala Ala Lys Gly Asn Ile Gln Leu
595 600 605

Arg Asn Thr Lys Leu Asn Ala Ala Lys Ala Leu Glu Thr Thr Ala Leu
610 615 620

Gln Gly Asn Ile Val Ser Asp Gly Leu His Ala Val Ser Ala Asp Gly
625 630 635 640

His Val Ser Leu Leu Ala Asn Gly Asn Ala Asp Phe Thr Gly His Asn
645 650 655

Thr Leu Thr Ala Lys Ala Asp Val Asn Ala Gly Ser Val Gly Lys Gly

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660	665	670
Arg Leu Lys Ala Asp Asn Thr Asn Ile Thr Ser Ser Ser Gly Asp Ile		
675	680	685
Thr Leu Val Ala Gly Asn Gly Ile Gln Leu Gly Asp Gly Lys Gln Arg		
690	695	700
Asn Ser Ile Asn Gly Lys His Ile Ser Ile Lys Asn Asn Gly Gly Asn		
705	710	715
Ala Asp Leu Lys Asn Leu Asn Val His Ala Lys Ser Gly Ala Leu Asn		
725	730	735
Ile His Ser Asp Arg Ala Leu Ser Ile Glu Asn Thr Lys Leu Glu Ser		
740	745	750
Thr His Asn Thr His Leu Asn Ala Gln His Glu Arg Val Thr Leu Asn		
755	760	765
Gln Val Asp Ala Tyr Ala His Arg His Leu Ser Ile Thr Gly Ser Gln		
770	775	780
Ile Trp Gln Asn Asp Lys Leu Pro Ser Ala Asn Lys Leu Val Ala Asn		
785	790	795
Gly Val Leu Ala Leu Asn Ala Arg Tyr Ser Gln Ile Ala Asp Asn Thr		
805	810	815
Thr Leu Arg Ala Gly Ala Ile Asn Leu Thr Ala Gly Thr Ala Leu Val		
820	825	830
Lys Arg Gly Asn Ile Asn Trp Ser Thr Val Ser Thr Lys Thr Leu Glu		
835	840	845
Asp Asn Ala Glu Leu Lys Pro Leu Ala Gly Arg Leu Asn Ile Glu Ala		
850	855	860

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Gly Ser Gly Thr Leu Thr Ile Glu Pro Ala Asn Arg Ile Ser Ala His
865 870 875 880

Thr Asp Leu Ser Ile Lys Thr Gly Gly Lys Leu Leu Leu Ser Ala Lys
885 890 895

Gly Gly Asn Ala Gly Ala Pro Ser Ala Gln Val Ser Ser Leu Glu Ala
900 905 910

Lys Gly Asn Ile Arg Leu Val Thr Gly Glu Thr Asp Leu Arg Gly Ser
915 920 925

Lys Ile Thr Ala Gly Lys Asn Leu Val Val Ala Thr Thr Lys Gly Lys
930 935 940

Leu Asn Ile Glu Ala Val Asn Asn Ser Phe Ser Asn Tyr Phe Pro Thr
945 950 955 960

Gln Lys Ala Ala Glu Leu Asn Gln Lys Ser Lys Glu Leu Glu Gln Gln
965 970 975

Ile Ala Gln Leu Lys Lys Ser Ser Pro Lys Ser Lys Leu Ile Pro Thr
980 985 990

Leu Gln Glu Glu Arg Asp Arg Leu Ala Phe Tyr Ile Gln Ala Ile Asn
995 1000 1005

Lys Glu Val Lys Gly Lys Lys Pro Lys Gly Lys Glu Tyr Leu Gln Ala
1010 1015 1020

Lys Leu Ser Ala Gln Asn Ile Asp Leu Ile Ser Ala Gln Gly Ile Glu
1025 1030 1035 1040

Ile Ser Gly Ser Asp Ile Thr Ala Ser Lys Lys Leu Asn Leu His Ala
1045 1050 1055

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Ala Gly Val Leu Pro Lys Ala Ala Asp Ser Glu Ala Ala Ala Ile Leu
1060 1065 1070

Ile Asp Gly Ile Thr Asp Gln Tyr Glu Ile Gly Lys Pro Thr Tyr Lys
1075 1080 1085

Ser His Tyr Asp Lys Ala Ala Leu Asn Lys Pro Ser Arg Leu Thr Gly
1090 1095 1100

Arg Thr Gly Val Ser Ile His Ala Ala Ala Ala Leu Asp Asp Ala Arg
1105 1110 1115 1120

Ile Ile Ile Gly Ala Ser Glu Ile Lys Ala Pro Ser Gly Ser Ile Asp
1125 1130 1135

Ile Lys Ala His Ser Asp Ile Val Leu Glu Ala Gly Gln Asn Asp Ala
1140 1145 1150

Tyr Thr Phe Leu Lys Thr Lys Gly Lys Ser Gly Lys Ile Ile Arg Lys
1155 1160 1165

Thr Lys Phe Thr Ser Thr Arg Asp His Leu Ile Met Pro Ala Pro Val
1170 1175 1180

Glu Leu Thr Ala Asn Gly Ile Thr Leu Gln Ala Gly Gly Asn Ile Glu
1185 1190 1195 1200

Ala Asn Thr Thr Arg Phe Asn Ala Pro Ala Gly Lys Val Thr Leu Val
1205 1210 1215

Ala Gly Glu Glu Leu Gln Leu Leu Ala Glu Glu Gly Ile His Lys His
1220 1225 1230

Glu Leu Asp Val Gln Lys Ser Arg Arg Phe Ile Gly Ile Lys Val Gly
1235 1240 1245

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Lys Ser Asn Tyr Ser Lys Asn Glu Leu Asn Glu Thr Lys Leu Pro Val
 1250 1255 1260

Arg Val Val Ala Gln Thr Ala Ala Thr Arg Ser Gly Trp Asp Thr Val
 1265 1270 1275 1280

Leu Glu Gly Thr Glu Phe Lys Thr Thr Leu Ala Gly Ala Asp Ile Gln
 1285 1290 1295

Ala Gly Val Gly Glu Lys Ala Arg Val Asp Ala Lys Ile Ile Leu Lys
 1300 1305 1310

Gly Ile Val Asn Arg Ile Gln Ser Glu Glu Lys Leu Glu Thr Asn Ser
 1315 1320 1325

Thr Val Trp Gln Lys Gln Ala Gly Arg Gly Ser Thr Ile Glu Thr Leu
 1330 1335 1340

Lys Leu Pro Ser Phe Glu Ser Pro Thr Pro Pro Lys Leu Ser Ala Pro
 1345 1350 1355 1360

Gly Gly Tyr Ile Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile
 1365 1370 1375

Glu Lys Leu Ser Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln
 1380 1385 1390

Val Ala Lys Asn Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Arg
 1395 1400 1405

Trp Asp Tyr Lys Gln Glu Gly Leu Thr Glu Ala Gly Ala Ala Ile Ile
 1410 1415 1420

Ala Leu Ala Val Thr Val Val Thr Ser Gly Ala Gly Thr Gly Ala Val
 1425 1430 1435 1440

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Leu Gly Leu Asn Gly Ala Ala Ala Ala Ala Thr Asp Ala Ala Phe Ala
 1445 1450 1455

Ser Leu Ala Ser Gln Ala Ser Val Ser Phe Ile Asn Asn Lys Gly Asp
 1460 1465 1470

Val Gly Lys Thr Leu Lys Glu Leu Gly Arg Ser Ser Thr Val Lys Asn
 1475 1480 1485

Leu Val Val Ala Ala Ala Thr Ala Gly Val Ala Asp Lys Ile Gly Ala
 1490 1495 1500

Ser Ala Leu Asn Asn Val Ser Asp Lys Gln Trp Ile Asn Asn Leu Thr
 1505 1510 1515 1520

Val Asn Leu Ala Asn Ala Gly Ser Ala Ala Leu Ile Asn Thr Ala Val
 1525 1530 1535

Asn Gly Gly Ser Leu Lys Asp Asn Leu Glu Ala Asn Ile Leu Ala Ala
 1540 1545 1550

Leu Val Asn Thr Ala His Gly Glu Ala Ala Ser Lys Ile Lys Gln Leu
 1555 1560 1565

Asp Gln His Tyr Ile Val His Lys Ile Ala His Ala Ile Ala Gly Cys
 1570 1575 1580

Ala Ala Ala Ala Ala Asn Lys Gly Lys Cys Gln Asp Gly Ala Ile Gly
 1585 1590 1595 1600

Ala Ala Val Gly Glu Ile Val Gly Glu Ala Leu Thr Asn Gly Lys Asn
 1605 1610 1615

Pro Asp Thr Leu Thr Ala Lys Glu Arg Glu Gln Ile Leu Ala Tyr Ser
 1620 1625 1630

Lys Leu Val Ala Gly Thr Val Ser Gly Val Val Gly Gly Asp Val Asn

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1635	1640	1645
Ala Ala Ala Asn Ala Ala Glu Val Ala Val Lys Asn Asn Gln Leu Ser		
1650	1655	1660
Asp Lys Glu Gly Arg Glu Phe Asp Asn Glu Met Thr Ala Cys Ala Lys		
1665	1670	1675 1680
Gln Asn Asn Pro Gln Leu Cys Arg Lys Asn Thr Val Lys Lys Tyr Gln		
1685	1690	1695
Asn Val Ala Asp Lys Arg Leu Ala Ala Ser Ile Ala Ile Cys Thr Asp		
1700	1705	1710
Ile Ser Arg Ser Thr Glu Cys Arg Thr Ile Arg Lys Gln His Leu Ile		
1715	1720	1725
Asp Ser Arg Ser Leu His Ser Ser Trp Glu Ala Gly Leu Ile Gly Lys		
1730	1735	1740
Asp Asp Glu Trp Tyr Lys Leu Phe Ser Lys Ser Tyr Thr Gln Ala Asp		
1745	1750	1755 1760
Leu Ala Leu Gln Ser Tyr His Leu Asn Thr Ala Ala Lys Ser Trp Leu		
1765	1770	1775
Gln Ser Gly Asn Thr Lys Pro Leu Ser Glu Trp Met Ser Asp Gln Gly		
1780	1785	1790
Tyr Thr Leu Ile Ser Gly Val Asn Pro Arg Phe Ile Pro Ile Pro Arg		
1795	1800	1805
Gly Phe Val Lys Gln Asn Thr Pro Ile Thr Asn Val Lys Tyr Pro Glu		
1810	1815	1820
Gly Ile Ser Phe Asp Thr Asn Leu Lys Arg His Leu Ala Asn Ala Asp		
1825	1830	1835 1840

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Gly Phe Ser Gln Glu Gln Gly Ile Lys Gly Ala His Asn Arg Thr Asn
 1845 1850 1855

Phe Met Ala Glu Leu Asn Ser Arg Gly Gly Arg Val Lys Ser Glu Thr
 1860 1865 1870

Gln Thr Asp Ile Glu Gly Ile Thr Arg Ile Lys Tyr Glu Ile Pro Thr
 1875 1880 1885

Leu Asp Arg Thr Gly Lys Pro Asp Gly Gly Phe Lys Glu Ile Ser Ser
 1890 1895 1900

Ile Lys Thr Val Tyr Asn Pro Lys Lys Phe Ser Asp Asp Lys Ile Leu
 1905 1910 1915 1920

Gln Met Ala Gln Asn Ala Ala Ser Gln Gly Tyr Ser Lys Ala Ser Lys
 1925 1930 1935

Ile Ala Gln Asn Glu Arg Thr Lys Ser Ile Ser Glu Arg Lys Asn Val
 1940 1945 1950

Ile Gln Phe Ser Glu Thr Phe Asp Gly Ile Lys Phe Arg Ser Tyr Phe
 1955 1960 1965

Asp Val Asn Thr Gly Arg Ile Thr Asn Ile His Pro Glu
 1970 1975 1980

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 acides aminés
- (B) TYPE : acide aminé
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

00228457.001401

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:1..143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Met Lys Asn Asn Ile Phe Leu Asn Leu Asn Lys Lys Ser Ile Asn Asn
1 5 10 15

Asn His Phe Val Ile Ser Ile Phe Phe Glu Thr Ile Tyr Gln Phe Glu
 20 25 30

Thr Lys Asp Thr Leu Leu Glu Cys Phe Lys Asn Ile Thr Thr Thr Gly
 35 40 45

His Phe Gly Val Ile Gly Ala Gln Tyr Glu Lys Ile Asp Ala Thr Arg
 50 55 60

Trp Ile Gly Asp Tyr Glu Glu Val Asn Gly Phe Glu Tyr Ile Asp Lys
65 70 75 80

Ala Pro Ser Ile Tyr Phe Ser Val Gly Asp Asp Phe Asn Pro Glu Glu
 85 90 95

Leu Ile Ile Pro Ile Asn Leu Ala Tyr His Tyr Phe Asn Ile Ala Ile
 100 105 110

Ser Asp Phe Leu Ile Ala His Pro Glu Tyr Gln Lys Lys Cys Lys Glu
 115 120 125

Ile Gln Lys Thr Tyr Ser Gln Thr Asn Cys Ser Leu His Glu Thr
 130 135 140

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(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 acides aminés
- (B) TYPE : acide aminé
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1..833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Val Leu Lys Thr Pro Pro Thr Leu Ala Ala Glu Leu Ser Gly Lys Thr
1 5 10 15

Gly Val Ser Ile Ser Ala Pro Tyr Ala Asn Glu Asn Ser Arg Ile Leu
20 25 30

Leu Ser Thr Thr Asp Ile Ser Ser Glu Asn Gly Lys Ile Lys Ile Gln
35 40 45

Ser Tyr Gly Asp Gln Tyr Tyr Tyr Ala Arg Gln Ser Glu Leu Tyr Thr
50 55 60

Phe Glu Arg Arg Ser Tyr Lys Thr Gly Lys Trp Tyr Asn Arg Lys His
65 70 75 80

Ile Thr Glu Val Lys Glu His Lys Asn Ala Lys Pro Asp Ala Val Asn
85 90 95

Leu Ser Ala Ser Gln Gly Ile Asp Ile Lys Ser Gly Gly Ser Ile Asp
100 105 110

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Ala Tyr Ala Thr Ala Phe Asp Ala Pro Lys Gly Ser Ile Asn Ile Glu
 115 120 125

Ala Gly Arg Lys Leu Thr Leu Tyr Ala Val Glu Glu Leu Asn Tyr Asp
 130 135 140

Lys Leu Asp Ser Gln Lys Arg Arg Arg Phe Leu Gly Ile Ser Tyr Ser
 145 150 155 160

Lys Ala His Asp Thr Thr Thr Gln Val Met Lys Thr Ala Leu Pro Ser
 165 170 175

Arg Val Val Ala Glu Ser Ala Asn Leu Gln Ser Gly Trp Asp Thr Lys
 180 185 190

Leu Gln Gly Thr Gln Phe Glu Thr Thr Leu Gly Gly Ala Thr Ile Arg
 195 200 205

Ala Gly Val Gly Glu Gln Ala Arg Ala Asp Ala Lys Ile Ile Leu Glu
 210 215 220

Gly Ile Lys Ser Ser Ile His Thr Glu Thr Val Ser Ser Ser Lys Ser
 225 230 235 240

Thr Leu Trp Gln Lys Gln Ala Gly Arg Gly Ser Asn Ile Glu Thr Leu
 245 250 255

Gln Leu Pro Ser Phe Thr Gly Pro Val Ala Pro Val Leu Ser Ala Pro
 260 265 270

Gly Gly Tyr Ile Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Gln Ile
 275 280 285

Glu Thr Leu Thr Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln
 290 295 300

09928457-081401

Val Ala Lys Asn Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Lys
305 310 315 320

Trp Asp Tyr Lys Gln Glu Gly Met Thr Pro Ala Ala Ala Val Val
325 330 335

Val Ile Val Val Thr Val Leu Thr Tyr Gly Ala Leu Ser Ala Pro Ala
340 345 350

Ala Ala Gly Thr Ala Gly Ala Ala Gly Ala Gly Ala Gly Gly Ala Ala
355 360 365

Ala Gly Thr Ala Ala Gly Thr Gly Val Ala Ala Gly Thr Ala Ala Thr
370 375 380

Thr Gly Val Ala Ala Gly Thr Ser Ala Ala Ala Ile Thr Thr Ala Ala
385 390 395 400

Gly Lys Ala Ala Leu Ala Ser Leu Ala Ser Gln Ala Ala Val Ser Leu
405 410 415

Ile Asn Asn Lys Gly Asp Ile Asn His Thr Leu Lys Glu Leu Gly Lys
420 425 430

Ser Ser Thr Val Arg Gln Ala Ala Thr Ala Ala Val Thr Ala Gly Val
435 440 445

Leu Gln Gly Ile Ser Gly Leu Asn Thr Gln Ala Ala Glu Ala Val Ser
450 455 460

Lys His Phe His Ser Pro Ala Ala Gly Lys Leu Thr Ala Asn Leu Ile
465 470 475 480

Asn Ser Thr Ala Ala Ala Ser Val His Thr Ala Ile Asn Gly Gly Ser
485 490 495

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Leu Lys Asp Asn Leu Gly Asp Ala Ala Leu Gly Ala Ile Val Ser Thr
 500 505 510

Val His Gly Glu Val Ala Ser Lys Ile Lys Phe Asn Leu Ser Glu Asp
 515 520 525

Tyr Ile Ala His Lys Ile Ala His Ala Val Ala Gly Cys Ala Ser Ala
 530 535 540

Val Ala Asn Lys Gly Lys Cys Arg Asp Gly Ala Ile Gly Ala Ala Val
 545 550 555 560

Gly Glu Met Val Gly Glu Thr Leu Leu Asp Gly Arg Asp Val Gly Lys
 565 570 575

Leu Ser Pro Gln Glu Arg Gln Lys Val Ile Ala Tyr Ser Gln Ile Ile
 580 585 590

Ala Gly Ser Ala Val Ala Leu Val Lys Gly Asp Val Asn Thr Ala Val
 595 600 605

Asn Ala Ala Thr Val Ala Val Glu Asn Asn Ser Leu Leu Ala Arg Arg
 610 615 620

Arg Val Asn Ile Arg Trp Thr Pro Arg Gln Glu Leu Glu His Glu Tyr
 625 630 635 640

Ala Ile Leu Glu Ile Gln Ala Ile Thr Asn Gln Ile Arg Arg Leu Asp
 645 650 655

Pro Lys Phe Asn Gly Ile Ala Ile Leu Arg Thr Pro Gly Glu Pro Trp
 660 665 670

Thr Arg His Asp Val Gln Thr Tyr Arg Gln Tyr Tyr Asn Gln Leu Arg
 675 680 685

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Glu Ser Arg Gly Phe Ala Val Glu Pro Ile Tyr Arg Ile Arg Ile Asn
 690 695 700

Asn Gly Asn Glu Phe Asn Arg Ile Met Ser Ser Lys Tyr Pro Tyr Asn
 705 710 715 720

Glu Leu Tyr Val Ala Asn Pro Lys Ser Ala Thr Gly Tyr Phe Arg Val
 725 730 735

Asp Ser Tyr Asp Pro Ala Thr Arg Glu Ile Ile Ser Arg Lys Phe Thr
 740 745 750

Gln Phe Ser Gln Ile Gln Glu Ser Thr Gly Ile Gly Tyr Ile Lys Glu
 755 760 765

Ala Val Arg Lys Tyr Ser Pro Gly Thr Val Ile Ser Asn Val Pro Ser
 770 775 780

Thr Pro Thr Thr Ile Arg Gly Arg Lys Leu Glu Gly Lys Leu Ile Leu
 785 790 795 800

Glu Val Pro Ala Gln Val Asn Pro Ile Pro Gln Ser Val Leu Arg Ala
 805 810 815

Ala Gln Glu Glu Asn Val Ile Ile Arg Asp Thr Thr Gly Arg Ile Tyr
 820 825 830

Lys

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 acides aminés
- (B) TYPE : acide aminé
- (D) TOPOLOGY : linear

09220457.1081404

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

	Met Lys Thr Ala Leu Pro Ser	
	170	175
Arg Val Val Ala Glu Ser Ala Asn Leu Gln Ser Gly Trp Asp Thr Lys		
	180	185 190
Leu Gln Gly Thr Gln Phe Glu Thr Thr Leu Gly Gly Ala Thr Ile Arg		
	195	200 205
Ala Gly Val Gly Glu Gln Ala Arg Ala Asp Ala Lys Ile Ile Leu Glu		
	210	215 220
Gly Ile Lys Ser Ser Ile His Thr Glu Thr Val Ser Ser Ser Lys Ser		
	225	230 235 240
Thr Leu Trp Gln Lys Gln Ala Gly Arg Gly Ser Asn Ile Glu Thr Leu		
	245	250 255
Gln Leu Pro Ser Phe Thr Gly Pro Val Ala Pro Val Leu Ser Ala Pro		
	260	265 270
Gly Gly Tyr Ile Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Gln Ile		
	275	280 285
Glu Thr Leu Thr Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln		
	290	295 300
Val Ala Lys Asn Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Lys		
	305	310 315 320
Trp Asp Tyr Lys Gln Glu Gly Met Thr Pro Ala Ala Ala Ala Val Val		
	325	330 335
Val Ile Val Val Thr Val Leu Thr Tyr Gly Ala Leu Ser Ala Pro Ala		
	340	345 350

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Tyr Ile Ala His Lys Ile Ala His Ala Val Ala Gly Cys Ala Ser Ala
530 535 540

Val Ala Asn Lys Gly Lys Cys Arg Asp Gly Ala Ile Gly Ala Ala Val
545 550 555 560

Gly Glu Met Val Gly Glu Thr Leu Leu Asp Gly Arg Asp Val Gly Lys
565 570 575

Leu Ser Pro Gln Glu Arg Gln Lys Val Ile Ala Tyr Ser Gln Ile Ile
580 585 590

Ala Gly Ser Ala Val Ala Leu Val Lys Gly Asp Val Asn Thr Ala Val
595 600 605

Asn Ala Ala Thr Val Ala Val Glu Asn Asn Ser Leu Leu Ala Arg Arg
610 615 620

Arg Val Asn Ile Arg Trp Thr Pro Arg Gln Glu Leu Glu His Glu Tyr
625 630 635 640

Ala Ile Leu Glu Ile Gln Ala Ile Thr Asn Gln Ile Arg Arg Leu Asp
645 650 655

Pro Lys Phe Asn Gly Ile Ala Ile Leu Arg Thr Pro Gly Glu Pro Trp
660 665 670

Thr Arg His Asp Val Gln Thr Tyr Arg Gln Tyr Tyr Asn Gln Leu Arg
675 680 685

Glu Ser Arg Gly Phe Ala Val Glu Pro Ile Tyr Arg Ile Arg Ile Asn
690 695 700

Asn Gly Asn Glu Phe Asn Arg Ile Met Ser Ser Lys Tyr Pro Tyr Asn
705 710 715 720

Glu Leu Tyr Val Ala Asn Pro Lys Ser Ala Thr Gly Tyr Phe Arg Val
725 730 735

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Asp Ser Tyr Asp Pro Ala Thr Arg Glu Ile Ile Ser Arg Lys Phe Thr
 740 745 750

Gln Phe Ser Gln Ile Gln Glu Ser Thr Gly Ile Gly Tyr Ile Lys Glu
 755 760 765

Ala Val Arg Lys Tyr Ser Pro Gly Thr Val Ile Ser Asn Val Pro Ser
 770 775 780

Thr Pro Thr Thr Ile Arg Gly Arg Lys Leu Glu Gly Lys Leu Ile Leu
 785 790 795 800

Glu Val Pro Ala Gln Val Asn Pro Ile Pro Gln Ser Val Leu Arg Ala
 805 810 815

Ala Gln Glu Glu Asn Val Ile Ile Arg Asp Thr Thr Gly Arg Ile Tyr
 820 825 830

Lys

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 acides aminés
- (B) TYPE : acide aminé
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1..162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Lys Lys Asp Ile Phe Tyr Cys Glu Gln Trp Ser Tyr Gly Tyr Lys
 1 5 10 15

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Arg Leu His Lys Pro Phe Ser Glu Lys Gln Ala Glu Glu Lys His Leu
20 25 30

Lys Gly Glu Leu Tyr Thr Ala Val Ile Gly Ser Ala Thr Gln Pro Glu
35 40 45

Tyr Val Ile Thr Leu Arg Glu Glu Val Gly Phe Phe Ser Val Asn Phe
50 55 60

Phe Asp Lys Phe Gly Arg Asp Tyr Leu Thr His Gln Phe Gln Lys Tyr
65 70 75 80

Ser Asn Ser Asn Tyr Tyr Phe Leu Ser Met Ala Val Trp Arg Asp Tyr
85 90 95

Ile Thr Leu Glu Ser His Asp Leu Ala Glu Gly Tyr Thr Tyr Phe Phe
100 105 110

Asn Glu Asn Thr Asp Asp Cys Tyr Val Leu Lys Gln Asp Phe Ile Asn
115 120 125

Asn Glu Arg Tyr Glu Lys Thr Glu Leu Tyr Ser Gln Lys Asp Lys Val
130 135 140

Ile Leu Phe Pro Lys Phe Gly Glu Tyr Asp Leu Val Leu Asn Pro Asp
145 150 155 160

Ile Ile

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 acides aminés
- (B) TYPE : acide aminé
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

099228457.081401

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:1..90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Met Asn Lys Arg Met Lys Met Cys Pro Ala Cys Gln Gln Gly Tyr Leu
1 5 10 15

Tyr His Ser Lys Pro Lys Tyr Leu His Asp Glu Ile Ile Leu Cys Asp
 20 25 30

Glu Cys Asp Ala Val Trp Leu Lys Gly Met Asn Ile Phe Tyr Gly Glu
 35 40 45

Tyr Glu Lys Asp Phe Tyr Ser Tyr Val Pro Phe Met Glu Ser Gln Gly
 50 55 60

Ile Thr Ser Glu Cys Ile Trp Glu Gly Asp Leu Phe Asp His Pro Tyr
65 70 75 80

Tyr Glu Asp Glu Asn Ser Asn Asp Met Asp
 85 90

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 acides aminés

(B) TYPE : acide aminé

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

09928457.081401

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:1..313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ser Ala Thr Glu Ile Glu Lys Ala Lys Ala Lys Ile Thr Ala Tyr
1 5 10 15

Ser Lys Leu Val Ala Gly Thr Ala Ser Ala Val Val Gly Gly Asp Val
20 25 30

Asn Thr Ala Ala Asn Ala Ala Gln Ile Ala Val Glu Asn Asn Thr Leu
35 40 45

Tyr Pro Arg Cys Val Gly Ala Lys Cys Asp Glu Phe Gln Lys Glu Gln
50 55 60

Gln Lys Trp Ile Arg Glu Asn Pro Glu Glu Tyr Arg Glu Val Leu Leu
65 70 75 80

Phe Gln Thr Gly Phe Ile Pro Ile Ile Gly Asp Ile Gln Ser Phe Val
85 90 95

Gln Ala Gln Thr Ala Ala Asp His Leu Phe Ala Leu Leu Gly Val Val
100 105 110

Pro Gly Ile Gly Glu Ser Ile Gln Ala Tyr Lys Val Ala Lys Ala Ala
115 120 125

Lys Asn Leu Gln Gly Met Lys Lys Ala Leu Asp Lys Ala Ala Thr Val
130 135 140

Ala Thr Ala Gln Gly Tyr Val Ser Lys Thr Lys Ile Lys Ile Gly Gln

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145 150 155 160
 Thr Glu Leu Arg Val Thr Ala Ala Thr Asp Lys Gln Leu Leu Lys Ala
 165 170 175
 Ile Gly Glu Gly Arg Asp Thr Thr Gly Lys Met Thr Glu Gln Leu Phe
 180 185 190
 Asp Ser Leu Ala Lys Gln Asn Gly Phe Arg Val Leu Ser Gly Gly Lys
 195 200 205
 Tyr Gly Gly Asn Asn Gly Phe Asp His Val Trp Gln Ala Ala Asp Gly
 210 215 220
 Ser Val Val Leu Ile Val Glu Ser Lys Gln Ile Arg Asn Gly Thr Val
 225 230 235 240
 Gln Leu Asn Pro Asn Gly Ala Gly Gly Tyr Thr Gln Met Ser Glu Asp
 245 250 255
 Trp Ile Arg Gln Val Leu Asp Gln Leu Pro Asp Gly Ser Pro Ala Lys
 260 265 270
 Ala Ala Val Phe Lys Ala Asn Lys Asn Gly Thr Leu Lys Thr Ala Ile
 275 280 285
 Ala Gly Val Asp Arg Gln Thr Gly Lys Ala Val Ile Leu Pro Val Lys
 290 295 300
 Val Pro Ser Lys Thr Asn Ile Arg Arg
 305 310

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

09928457.081401

- (A) LENGTH: 311 acides aminés
- (B) TYPE : acide aminé
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1..311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Met Gly His Asn Met Met Thr Thr Gln Lys Trp Tyr Glu His Ile Thr
1 5 10 15

Asn Val Ile Ile Gly Asn Thr Ala Asn Phe Asn Ser Gly Cys Leu Asp
20 25 30

Ser Ile Asp Tyr Val Asp Glu Arg Lys Gly Val Pro Leu Ala Ala Met
35 40 45

Gln His Ile Phe Met Asp Val Arg Ala Ala Ala Ser His Ala Tyr Leu
50 55 60

Phe Glu His Asp Leu Lys Lys Phe Lys Gln Tyr Ala Tyr Val Ala Gly
65 70 75 80

Lys Leu Gly Val Leu Leu Ser Val Asn Ser Thr Asp Pro Glu Pro Phe
85 90 95

Phe Phe Pro Cys Asp Met Leu Asn Ile Gln Asn Pro Met Phe Leu Met
100 105 110

Leu Met Ser Asp Ser Pro Gln Leu Arg Glu Phe Leu Val Arg Asn Ile
115 120 125

09928457.081401

Asp Asn Ile Ala Asn Asp Thr Glu Ala Phe Ile Asn Arg Tyr Asp Leu
 130 135 140

Asn Arg His Met Ile Tyr Asn Thr Leu Leu Met Val Glu Gly Lys Gln
 145 150 155 160

Leu Asp Arg Leu Lys Gln Arg Ser Glu Lys Val Leu Ala His Pro Thr
 165 170 175

Pro Ser Lys Trp Leu Gln Lys Arg Leu Tyr Asp Tyr Arg Phe Phe Leu
 180 185 190

Ala Phe Ala Glu Gln Asp Ala Glu Ala Met Lys Ala Ala Leu Glu Pro
 195 200 205

Leu Phe Asp Lys Lys Thr Ala Arg Met Ala Ala Lys Glu Thr Leu Ser
 210 215 220

Tyr Phe Asp Phe Tyr Leu Gln Pro Gln Ile Val Thr Tyr Ala Lys Ile
 225 230 235 240

Ala Ser Met His Gly Phe Asp Leu Gly Ile Asp Gln Glu Ile Ser Pro
 245 250 255

Arg Asp Leu Ile Val Tyr Asp Pro Leu Pro Ala Asp Glu Tyr Gln Asp
 260 265 270

Ile Phe Asp Phe Met Lys Gln Tyr Asp Leu Ser Tyr Pro Tyr Glu Tyr
 275 280 285

Leu Gln Asp Trp Ile Asp Tyr Tyr Thr Phe Lys Thr Asp Lys Leu Val
 290 295 300

Phe Gly Asn Ala Lys Arg Glu
 305 310

09928457.081401

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GCCACCGGTA CGGAAACTGA A

21

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CCTGAATTCA TGTCTATTCC ATTTTGAAGA

30

(2) INFORMATION FOR SEQ ID NO: 48:

09928457.081401

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

CCGAGATCTT TAACCCTTTG GGCTTAAGCG A

31

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GGGAGATCTC CCGCTCGTGT TGTGCATTA

29

09926457.081401

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

AAGAGATCTG CAGCCAAGGC TCTCGAAA

28

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GGGAGATCTC AGGCTGCCGC CGTTGA

26

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(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

GGGAGATCTC ACCCCAAGAA CGCCAAAA

28

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGGAGATCTG AACGTATAGT AATCTATCCA A

31

T04T00" 2542660

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

AGTGGCTCCT AG

12

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

T04T90"05457"081401

AGCACTCTCC AGCCTCTCAC CGAG

24

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

AGTGGCTCTT AA

12

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

0928457.081401

AGTGGCTGGC

10

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AGCACTCTCC AGCCTCTCAC CGAC

24

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

09928457.081401

GTACTTGCCT AG

12

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

ACCGACGTCG ACTATCCATG AACG

24

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

09020457.084401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GTACTTGCTT AA

12

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GTACTTGGGC

10

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

0928457.081401
10480.75482660

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ACCGACGTCG ACTATCCATG AACC

24

(2) INFORMATION FOR SEQ ID NO: 64

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

AATTCTCCCT CG

12

(2) INFORMATION FOR SEQ ID NO: 65

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

09923457-081401
T04T90-45492660

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AGGCAACTGT GCTATCCGAG GGAG

24

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GATCAACTTT TCCCTGTTTG TCCCATTACC GGTTTGAATG AACCGATTGC GCGCCGCGCG 60

TGTTGTTGGA CATTACCTGC GATTCAGACG GTACGATTGA CCACTACATC GAGGAGAACG 120

GCAATCAGGG TACAATGCTA 140

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE : nucleotide

0920457.081401

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GATCCGCGTA CTTGGTTTTT CATATTTTGC ATAGTCTTGT CGGTCGGGCA TCTTCCCCGA	60
CATCATCTAA ATTTGTCTTT ATTGGTTTTT ACGCCACTCA TTGCGGATAA ACAATATTCC	120
GCCTTGCCGT CGCGAATGTT CAAGCTAGCC TGCATCACC G TAATCAGGTT GCCCGTTACC	180
GAGCCTTCGA GA	192

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

GATCCGGCTG CCCGACGCGC GCAAAATTGC CGCCGAGGAA AGCGCGCACA ACCACGACGG	60
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09928457.081401

CAAAACCAGC GTATGGCAAT ACAAACATCT CGTGTCGGT ACGGCAGGCA TTTTCTGCTA 120
 TGTCGGCGCG GAGGTGTCTA TCGGTTCGTT GATGGTCAAC GTATTGGGTT ATCTGAAAGG 180
 GCTGGATC 188

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GATCCCCCAC TTTACCTCGG GCAGATTTTG CGCGTTCATT ACAATAGCGT ATTTATGCGT 60
 TTGCGTTTGC GCTTGCCGCT GCCCCCCCC CGCCGGTATG GGAAAACATC AATATGGCGG 120
 TATAAAGCGC GGTATGGCGG AAAACCTGCC GTTCCAAGT TTTATTCATC TTTTATTCCT 180
 TGAGTTTGCC TTCACGGGAC GGGGCGGCGC GCGGAACGCG GGGTTCGGTA AACCGCCCGA 240
 TTCCGCGCCC GCCGAATTGC TGATTGAAAA GCTTACTTCC CCAATTTAAC TTTGCACACT 300
 GATC 304

09928457.081401

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GATCAGACCC ATTTTCAGCG CACCGTAAGC GCGGATTTTC TCGAATTTTT CCAAAGCTGC	60
GGCATCGTTG TTGATGTCGT CTTGCAACTC TTTGCCCGTG TAGCCCAAGT CGGCGGCATT	120
CAGGAAAACG GTCGGAATGC CCGCGTTGAT GAGCGTGGCT TTCAAACGGC CTATATTCGG	180
CACATCAATT TCATCGACCA AATTGCCGGT TGGGAACATA CTGCCTTCGC CGTCGGCTGG	240
ATC	243

(2) INFORMATION FOR SEQ ID NO: 71

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

09928457.081401

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CGGCGGCGTA GTCCGCCGCG ACAGCGTTAC CATAAGCGGG ACAGACTACA CCCCTTTATC	60
TAACCCGCAA AGTTTGGATA CGGAATTAAA ATGGTTGCTT CAAGAAGCTC CCGAAATAGA	120
AAATCCTTTC GACCGCGCCG TTTATCTCCA TAATAATTTG GCGTATCTTC AATATTTTAA	180
AGATTGCAAT AAACGTACTG CCAGAACTG CATGACCTTG TCGTGATGC GCTCCG	236

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

CGGTCAATCA CAAGAAAGTC AGCCGTCTGA TGGCGAAGAC GGGGCTGAAG GCAGTGATAT	60
GGCGGCGCAA ATACCGCTCG TTCAAAGGAG AAGTCGGCAA AATTGCGCCG AATATCCTGC	120
GACGCTGTTT CCATGCAGAA AAGCCGAATG AGAAATGGGT AACGGACGTT GCCGAGTTCA	180
ATGTAGGCGG AGAAAAGATA TACCTTTCTC CGATTATGGA TTTGTTTAAC GGGGAAATCG	240

T04T80" 45432650

TCAGTTACCG TATTCAGACC CGCCCGACTT TCGATTGGC

280

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CGGTCAGAAA CAGGCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA 60

ACTCCTTACC GAAGTCTTCT ATACCCAGGC TCAATAGCCG CTCAAGGAGA GAGCTATCAT 120

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

0926457.081401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

CGGTCAGAAA CAGGCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA 60

ACTCCTTACC GAAGTCTTCT ATACCCAGGC TCAATAGCCG CTCAAGGAGA GAGCTATCAT 120

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CGGTGTTTTT CTTAACAATT CGCCGACTTC ATGGCGATAT TTAAGTGACA GTTGCTCCGC 60

CCACGCAGTT GCGCCGAAC T CAGCACCACG ACATTATACT GATTATGCAC ATCGGCAAGA 120

TCAAAC TGAC CTATCGTAGT ATCGCAGACT GT 152

(2) INFORMATION FOR SEQ ID NO: 76

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

09926457.081401

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CGGGAGGTTT TGTGCATCCT GATACCGATC GGTGTTGTT GCTCAAAGGA CAGAAGGCCG	60
CTGATAAACG AGATTACCTG TTTGTCGCTA TTGACGATTT TTATACTCTG CCATTTTGCC	120
AGACAAAACC GCAGACAGTG CTGCCAAGTT TCTGACCGAA CATCTGGCCG ACCCCTGCTT	180
GTACCTGATT GAGTACGCTT ACTCTGACAA TGATAGGTAA TATAAAGAGC CGTCCAACAT	240
GCTTTCGGTG CAGTTTGTTA TGATAATGGG ATTGGTTGGA GGCTTGCCCG ATTTGCTTGT	300
CCGCAGACCA ACGGTAAGGC GGAGCGGGTT ATCCGTACCT TGATGGAGAT GTGGCATGAG	360
GAACAGTCGT TTGACAGACC G	381

(2) INFORMATION FOR SEQ ID NO: 77

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

09928457.081401

CGGAGCATAA AATCGTTATT AAAGATAATG GTATAGGAAC GAGCTTCGAT GAAATCAATG 60

ATTTTTATTT GAGAATCGGT CGGAACAGAA GGGAAGAAAA ACAAGCCTCC CCGTGCGGAA 120

GAATTCCAAC GGGTAAAAAA GGCCTTGGTA AATTGGCATT ATTCGGGCTT GGCAACAAAA 180

TTGAAATTC TACTATCCAG GGAAACGAAA GGGTTACTTT TACTTTGGAT TATGCAGAGA 240

TTCGAAGAAG CAAGGGTATT TATCAACCG 269

(2) INFORMATION FOR SEQ ID NO: 78

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

CGGATGAAAA CGGCATACGC GCCAAAGTAT TTACGAACAT CAAAGGCTTG AAGATACCGC 60

ACACCTACAT AGAAACGGAC GCGAAAAAGC TGCCGAAATC GACAGATGAG CAGCTTTCGG 120

CGCATGATAT GTACGAATGG ATAAAGAAGC CCGAAAATAT CGGGTCTATT GTCATTGTAG 180

ATGAAGCTCA AGACGTATGG CCG 203

(2) INFORMATION FOR SEQ ID NO: 79:

0928457.081401

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

CGGTTTCAGG TTGTCGCGAA GGCTCGGTAA CGGGCAACCT GATTACGGGT GATGCAGGCA	60
GCTTGAACAT TCGCGACGGC AAGGCGGAAT ATGTTTATCC GCAATGAGTG GCGTAAAAAC	120
CAATAAAGAC AAATTTAGAT GATGTCGGGG AAGATGCCCG ACCGACAAGA CTATGCAAAA	180
TATGAAAAAC CAAGTACGCG GATCAGGCAT GGATGCACGA TCCAATCCG	229

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

0922457-081404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTTT GGCTTGACAG TTTGGAAATA 60
 TTGTGTATCG GGGGGGGGTA TTTGCTGACG TAAAAAACTA TAAACGCCGC GCAAATATG 120
 GCTGACTATA TTATTGACTT TGATTTTGTG CTGCGCGGTG ATGGATAAAA TCGCCAGCGA 180
 TAAAGAATTT GCGAGAACCT GATGCCG 207

(2) INFORMATION FOR SEQ ID NO: 81 :

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CGGCAACGAT TTGAGCTATC GCGGTTACGA CATTCTGGAT TTGGCACAAA AATGCGAGTT 60
 TGAAGAAGTC GCCCACCTGC TGATTCACGG CCATCTGCCC AACAAATTCG AGCTGGCCGC 120
 TTATAAAACC AAGCTCAAAT CCATGCGCGG CCTGCCTATC CGTGTGATTA AAGTTTTGGA 180
 AAGCCTGCCT GCACATACCC ATCCGATGGA CGTAATGCGT ACCG 224

(2) INFORMATION FOR SEQ ID NO: 82:

09928457.081401
 T04T80.45482660

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CGGGAACAGC CATTGCCCAC GCCCAGCCCC CCAAGAAAG ACGGAACTA CTGCCTAAAT	60
TTTCGGCAAT CAAGTTGACG ATTAAAGGGT TGGGGGCAGT TGCAGTAATA AACATAGCCG	120
ACGAAATGGG ATTGGAATGA TAGTTGACCA AAGCCAAATA TTTACCCATC TTGCCTTCTG	180
TGCCTTTTGC GGGATTGGAG CCGTAACTGC CG	212

(2) INFORMATION FOR SEQ ID NO: 83

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

09920457.061401

CGGGAATTCT GAGCAGAATG AAAGAAAGCA GGCTTGATAA TTTCATAAAG TTATTGGAAG 60

AAAAAGGATT TACCGTCCAT TTCGGTATTC ACAATACGGC TGATTACGGA ATTCCCCAAA 120

GCCGTAAAAG ATTTACGTTA ATTGCAAACA GAATAACCAA AGAAAAGCTG GAACCACTCA 180

AGTATTCGGG CAAACGGCTT ACGGTAGCCG ATGTTTTGGG AATGGAAATG GCTTTCCCAA 240

CATTATTGCA GGACACCAAG ACGAAACGGA TTTTATGCAT AGCTGTGCGG GAATTATCTG 300

ATATCACTTG AACGATTGGC TTGATACCTA AAAACGGAGG AACCGTTGGC TTT 353

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

AATTCGGTAT CCAAACCTTG CGGGTTAGAT AAAGGGGTGT AGTCTGTCCC GCTTATGGTA 60

ACGCTGTGCG GCGGGACTAC GCCCGGAGCC TTTTCCAGT AAGTTTTTCGG AAATCAGGCT 120

GTGGGTGGTT TTTAAGAAAT CCAACCAGTC AAACGGCTCG GGGCTGTCCA AACCGGACAC 180

AGGTGCCGGT AACTTTCCCT CAGGTTGATT AACATTACGG CATCCGAATA TAACTTCCCG 240

09928457.081401

CCTGCGGTTT GCCCGAGTTT AAGCAATGCC TCGTATCGT ATTGATTATA AAGTGTTTCC 300
 TTCCAATT 308

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

AATTCGTGTG CCGCGTCGAC AAACCGCTGA CGTAGCGGAT GTCTCATGCC ACGTTTCAAA 60
 GCAGGTTGAT GGCGGTTAGC AACCTCTGA TTCACTGGG ATAT 104

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

05923457.DBT404
 104190/4542650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

AATTGCGTAG AGTGGGCTTC AGCCACGTTT TTCTTTTTTC GGTCGTTGAT TGGTGGGCTG 60

AACCACTTGT TTCGGAAATC CGTATCATG 89

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

AATTTCCACC TATGCCCTAC GCAGCGATTA TCCGTGGTTT ACCCAAAGGG TGATTATGGC 60

AAAAGCGCGG GGTGAGCGA CCGCCTTTTG TTGCCGGCGT TCAAACGGGT TTTGATAGGA 120

AATGCAGGCA CGAAGCCTCG GCTGATTGTG ATGCACCTGA TGGGTTCGCA CAGTGATTTT 180

TGCACACGTT TGGATAAGGA TGC GCGGCGG TTT CAGTATC AA ACTGAAAA AATATCCTGC 240

TATGTTTCCA TCAATCGCGC AAACCGATAA ATT 273

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs

09923457-081401
F04T80-25432660

- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

AATTCTTCCG CACGGGGAGG CTTGTTTTTC TTCCCTTCTG TTCCGACCGA TTCTCAAATA	60
AAAATCATTG ATTTTCATCGA AGTTCATTCC TATACCATTG TCTTTAATAA CGATTTTATG	120
CTCCGGTTTA TCGAATAACC TAACTTCCAC TTCCGTAGCA CATGCATCGT AGGCATTTCGC	180
TATCAACTCG GCAATCGCAG GAACAGTGTG CGAATACAAT CTTTACACCC AAATGTTTGA	240
TTACGGTTGG CTCGAAACTC AATTTCAATT	270

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE : nucleotide
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

09926457.081401

AATTATGAAC ACACGCATCA TCGTTTCGGC TCGTTCGTT GCGTTGGCAT TAGCAGGTTG 60
 CGGCTCAATC AATAATGTAA CCGTTTCCGA CCAGAACTT CAGGAACGTG CCGCGTTTGC 120
 CTTGGGCGTC ACCAATGCCG TAAAAATCAG CAACCGCAGC AATGAAGGCA TACGCATCAA 180
 CTTTACCGCA ACTGTGGGTA AGCGCGTGAC CAATGCTATG TTACCAGTGT AATCAGCACA 240
 ATCGGCGTTA CCACTTCCGA TGCAATT 267

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

AATTTTATT TGGTTCGTAG TCATTTTGTG CAACTGAACG ATATTCGTTT TCATCATTGC 60
 TAACGTCTAG TGCCCATTGT GGCCCGTAAT AAGAGATTTT GTCTCCTTTT ACATGTTTGA 120
 CGCTGACGGC AACTGAGGGA TCGATGACGG ATAATGTACG TCTGTTGACA TCTGCAACGC 180
 TAAATCAATC ATCGGTATTG GATAATGCGT TGCCGATGTT TTGACTTGTA TGTT 234

(2) INFORMATION FOR SEQ ID NO: 91:

09928457-081401

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

AATTCGGCCG GCTGTGTCAA ATAATGCGTT ACTTTGGCCG GGTCTGTTC TTTGTAAGTG	60
GTGGTCTTTT TTTGCGCGTT ATCCCCATCT GTTTGAGTGC ATAGCAAATG GTGGCTGCCG	120
TACAATCAAA TGTTTGGCGT TCATGCAGAT AGGCATCATG GTTTGCCCA ATATATTGAG	180
CCGGTTTTTG CCTATCCGAT TTGACGGCAT TTAGACCGGT AACTTGATGT TTTAAGCTGC	240
CTGTTTGTTT AAAGGCGAAT CCACAAGTAA AGCGTGTTTC TTGACAGGTT AAACG	295

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

09928457.081401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

AATTGTGTAT ATCAAGTAGG ATGGGCATTT ATGCCTGACC TACAAAACCA AAAACAACCT 60
 ACCACCCTTA ATCAACTCCA CAAACCCTCT TCAGACAACC TCGTTTTTTG AAAACAATC 120
 TGTAACAGA TAACTGCTGA AGAATACCGT TGCCGAGCCC CAAAACCCGT ACTGCAACTT 180
 TTATTGTGAA CTTCCCATTA TGAGAAAATC CCTTTTCGTC CTCTTTCTGT ATTGTCCTCT 240
 ACTTACTGCC AGCGAAATT 259

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

AATTGCACCA CGCGATGATG GGTACGCCTC TGTTGCCATT GCGACCGCCG CCGCCGTGCC 60
 CCGTACGCTG GTCAACCTTG CCGCGGCGGA ACGGGTAAAG AAGTGCGCTT CGGGCATCCT 120
 TCCGGTACAT TGC GCGTCGG TGCAGCGCCG AATGTCAGGA CGGACAATGG ACGGCCACCA 180
 AAGCGGTTAT GAGCCGCAGC GCACGCGTGA TGATGGAAGG TTGGGTCAGG GTGCCGGAAG 240

09928457-081401
 104180-25482660

ATTGTTTTTA AATTGGACGG CGAACCGGTC TATTCGTATT GCGGTTATAC CGCCGCAAAG 300
 GCAGACCTTG AACTGGTGC GTGCCGTGCA GGGCATGTAC GGCTATGTGT GCGTGGCGGG 360
 CGGATTTGAT GTGCGGAAT 379

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

AATTTGTTGG GCAGATGGCC GTGAATCAGC AGGTGGGCGA CTTCTTCAAA CTCGCATTTT 60
 TGTGCCAAAT CCAGAATGTC GTAACCGCGA TACGTCAAAT CGTTGCCGGT ACGCAACGGT 120
 ACACAAAGCG GTATTACCGG CCGCAACGCC AGAAAGCGCA ACGGATTTTT AGGTTTGAGG 180
 GTCGGGGTTT GAGTAGTTTC AGTCATGGTA TTTCTCCTTT GTGTTTTTAT GGGTTTCGGG 240
 TTTTCAGACG ACCGATGCGG ATTTGTGTA AGGCAGTCTG AAAGCGGTAA ATCATTTTTG 300
 AAACAATT 308

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

09026457.081401

- (A) LENGTH: 286 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AATTCGGAGG AGCAGTACCG CCAAGCGTTG CTCGCCTATT CCGGCGGTGA TAAACAGAC	60
GAGGGTATCC GCCTGATGCA ACAGAGCGAT TACGGCAACT TGTCTACCA CATCCGTAAT	120
AAAAACATGC TTTTCATTTT TTCGGCAAGC AATGACGCAC AAGCTCAGCC CAACACAACT	180
GACCCTATTG CCATTTTATG AAAAAGACGC TCAAAAAGGC ATTATCACAG TTGCAGGCGT	240
AGACCGCAGT GGAGAAAAGT TCAATGGCTC CAACCATTCG GGAATT	286

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

09928457.081401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

AATTTGGATA CGTTGGAAAA GGGATATTTG ATTGGGAATG GGATGAAGAT AAGCGTAGAT 60
 GAGTTGGGGA AAAAAGTGTT AGAACATATC GGTAAGAATG AACCGTTATT GTTGAAAAAT 120
 CTACTGGTTA ACTTCAATCA GGGAAAACAT GAAGAAGTTA GGAAGTTGAT TTATCAGTTG 180
 ATAGAGTTAG ATTTTCTGGA ACTTTTGTGA GGGATTCTAT GAAAACTGG AAGCAATT 238

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

AATTCGGCAC GCAGGTTTTT TAAAAAAGG CCGTTGATGA CTTTGTGAT ATTGGCGGCT 60
 TCGGTGTAGT GCGCGCCCGC TTCGGCCGCT CTTGCGCGTC CATGACGGAT TGAAGAGCG 120
 TGCCGAAGAT TTCTGGACTG ATGTTGCGCC AGTCGAAATT GCCGACACGG GAGGAATACC 180
 TGCCAACAAG AGTGCAGGCA GCGTAATCAA ACCACCCCA CCGCAATCG CATCGATAAA 240
 TCCGGCAATC ATCGCAACCA AACCCAAAGC GAGTATTATG TATAAATCTT CCATGTTTCT 300
 TAATCCTGTT AACTTGCACC AA 322

09026457.031401
 204907549550

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98

AATTTGTCGG CAATCTTCCC GGGTCGCTTT ATTTTGTGCA GGCATTATTT TTCATTTTTG 60
 GCTTGACAGT TTGGAGATAT TGTGTATCGG GGGGGGGTAT TTGCTGACGT AAAAAACTAT 120
 AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTG CTGCGCGGTG 180
 ATGGATAAAA TCGCCAGCGA TAAAGATTTG CGAGAACCTG ATGCCGGCCT GTTGTGAAT 240
 ATTTTCGACC TGTAATTACG ATTTGGCTTC CGCGCCGGCA CAATATGCCG CCAAGCGGCG 300
 CCCACATTTT GGAAGC 316

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

0928457-081401

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

AATTCGGACA GTATGAATAC AGCGGATTAA TACAAGGTAA GTTCATTACA ACGGAAAAAC	60
CTTTAAAGAA TAATATGAAA GGTATTACCT TGTTTGCCAA CGGGAATGGT AAATATGCCC	120
GAGTTTTTCA CTGAATAGCG AATCCAGCCA TTTCTATTCA TATTTGACTG GATGGCTGAA	180
TGTGGACTTT ATAGATAATG ACGATGAAGA TTTAATT	217

09928457.081401